









































CC 60669 as claimed. A method to isolate nucleic acid fragments encoding fatty acid desaturase and related enzymes is claimed which comprises: comparing At cDNA probes to AF0497, AF0792 and other fatty acid desaturase sequences; identifying conserved sequences of 4 or more AAs; designing degenerate oligos based on the conserved sequences; and using the oligos to amplify sequences encoding fatty acid desaturase and desaturase related enzymes.

Sequence: 383 AA

Query Match 89.5% Score: 2004, OR 10%, Length: 383  
Best local similarity: 91.4% Pos: 4, CDS: 255  
Matches: 351, Conservative: 8, Mismatches: 24, Indels: 1, Gaps: 1

Db 1 mngagmgpspskscsdhkrpccpffvga-llh-afphstksfstslwt-60  
1 MGAGCMWVSPSKSEETDINKVCEHTFEVGLKNAIFPHFSRSEFSESLWML 60  
QY 1  
Db 61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
QY 61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
Db 121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
QY 121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
Db 180 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 239  
180 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 239  
QY 181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
QY 181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
Db 240 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 299  
240 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 299  
QY 241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
QY 241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
Db 300 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 359  
300 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 359  
QY 301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
QY 301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
Db 360 keciyepdrgqekkytwynkl 383  
360 keciyepdrgqekkytwynkl 383  
QY 361 keciyepdrgqekkytwynkl 384  
361 keciyepdrgqekkytwynkl 384

## RESULT 2

ID R53697 standard; Protein: 383 AA.  
AC R53697  
DT 09-NOV-1994 (first entry)  
DE Sequence of microsomal delta-12 desaturase.  
KM Fatty acid desaturase; lipid; unsaturated; transgenic plant.  
OS Arabidopsis thaliana.  
PN W09411516 A.  
PD 26 MAY 1994.  
PF 15-OCT-1993; 009961.  
PR 17-NOV-1992; US 971333.  
PA (DDPO ) DU PONT DE NEMOURS & CO E. I.  
PI Lightner JE, Okuley JJ  
DR WPI 94-183519/22.  
DR N-FSD8; 066068.  
PT Genes for fatty acid desaturase enzymes patent application of  
PT Plant lipid composition  
PC Claim 13; Page 112-114; 147pp; English.  
CC The gene codes to 066068 was isolated by screening Arabidopsis  
CC genomic DNA library using radiolabeled cDNA insert, putting  
CC positively-hybridizing plaques, and subcloning a 6kb Hind III insert  
CC fragment from the phage DNA in phoscript vector. Comparison of the

CC sequences of the gene (G6672) and the cDNA (G6672) revealed the  
CC presence of a single insertion of 1134 bp at a position between  
CC nucleotides 88 and 89 of the cDNA, which is 4 bp before the  
CC initiation codon. A method to isolate nucleic acid fragments  
CC encoding fatty acid desaturase and related enzymes is claimed  
CC which comprises: comparing the sequences of AF0497, AF0792 and other  
CC fatty acid desaturase cDNA sequences; identifying conserved  
CC sequences of 4 or more AAs; designing degenerate oligos based on  
CC the conserved sequences; and using the degenerate oligos to isolate  
CC sequences encoding fatty acid desaturase and related enzymes.

Sequence: 383 AA

Query Match 89.4% Score: 2004, OR 10%, Length: 383  
Best local similarity: 88.5% Pos: 1,360 254  
Matches: 340, Conservative: 23, Mismatches: 20, Indels: 1, Gaps: 1

Db 1 mngagmgpspskscsdhkrpccpffvga-llh-afphstksfstslwt-60  
1 MGAGCMWVSPSKSEETDINKVCEHTFEVGLKNAIFPHFSRSEFSESLWML 60  
QY 1  
Db 61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
QY 61 llaecfyvactyplllpmlsylvpmywaagcvllgwwahocghaalsdyqldd 120  
Db 121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
QY 121 tvgllfhsfllyfkwysrlthhstjelerdewpr-sqssgtastrfrrv 170  
Db 180 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 239  
180 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 239  
QY 181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
QY 181 mltvqllmwllylafvsgfpydrt-ahfpnapiydrfqlvlsdqlavayal 240  
Db 240 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 299  
240 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 299  
QY 241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
QY 241 lgyaaagmasmactyqypillmalvlllylqthpslphyssewawtjatrdr 300  
Db 300 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 359  
300 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 359  
QY 301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
QY 301 dygllnkvthltdehvalhstfmpvnaeatkaikpllgdyqldfpyvanyrea 360  
Db 360 keciyepdrgqekkytwynkl 383  
360 keciyepdrgqekkytwynkl 383  
QY 361 keciyepdrgqekkytwynkl 384  
361 keciyepdrgqekkytwynkl 384

## RESULT 3

ID P95579 standard; Protein: 384 AA.  
AC P95579  
DT 10-SEP-1996 (first entry)  
DE Kappa fatty acid hydroxylase Lesquerolus acid; transgenic plant;  
KM Kappa fatty acid hydroxylase; Lesquerolus acid; transgenic plant;  
KM oilseed seed oil; rapeseed; Canola; Brassica juncea; var. 134;  
KM oilseed seed oil; rapeseed; Canola; Brassica juncea; var. 134;  
KM oil palm corn.  
OS Lesquerella fendleri.  
PN W09410075 A1.  
PD 04 APR 1996.  
PF 25 SEP 1995; 011855.  
PR 26 SEP 1994; US 514506.  
PP 11 OCT 1994; US 520082.  
PE 20 SEP 1995; US 520082.  
PA (BR097) BR097 P.  
PA (GOME) GOMEVHLE C.  
PA (V1007) VAN DE DUN P. J.







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FD      26 MAY-1994.
PR      15-OCT-1993; 009987.
PA      (DUPFO ) DU PONT DE NEMOURS & CO E. I.
PI      Lightner JE, Okuley JJ;
DR      WP17 94-183515/22.
DT      R-F5C8; G66071.
PT      Genes for fatty acid desaturase enzymes - permit alteration of
FT      plant lipid composition.
PC      Ciam 13; Page 124 126; 14ppr English.
CC      Corn microsomal delta 12 desaturase cDNA was isolated using a PCR
CC      approach. A cDNA library was made to fully A MPRA from developing
CC      corn embryos. This library was used as template for PCR using sets
CC      of degenerate oligos S05 (G66073) and K5A/B (G66077,G66078) as
CC      sense and antisense primers, respectively. NC8 and RPNA/R (R5307P
CC      to stretches of Abc 101-162 and J16 325). Insertionally, of R53047,
CC      which are conserved in most microsomal delta-12 desaturases. A PCR
CC      product of D12bp was purified and used as a probe for screening the
CC      corn cDNA library. A plaque was purified and found to encode
CC      microsomal delta-12 desaturase truncated at the 3' end. This cDNA
CC      was used to probe the corn cDNA library again. The clone coding
CC      the longest insert, designated p42-1 was sequenced completely
CC      (G66071). An isolated nucleic acid fragment
CC      wherein the nucleic acid identity is 93% or greater to
CC      G66071 is claimed. A method to isolate nucleic acid fragments
CC      encoding fatty acid desaturases and related enzymes is claimed
CC      which comprises: comparing AA sequences in Genbank R53072 and other
CC      fatty acid desaturase sequences, identifying conserved sequences;
CC      4 or more AAs designed degenerate oligos based on the conserved
CC      sequences; and using the oligos to screen sequences encoding fatty
CC      acid desaturases and desaturase related enzymes.
CO      Sequence 387 AA;
CO      Query Match 66 467 6606 6607 6608 6609 Length 367;
CO      Best Local Similarity 68.66; Ident. No. 1,400-184;
CO      Matches 264; Conservative 46; Mismatches 68; Indels % Error 3;
DB      7 mtekerereqgaratgagtgamqspvckprptlgtgkkaipnctervsktslywbd 66
GY      1 MGAGSMMVGGESYKFKLSTFECVET TTTTTCG CGATGSGTGTSTSPSTLTMT 60
DB      67 viaaallvfatlnfpalselylamplwiaggovctgvwtiaohocghafsygl 176
GY      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      61 IIASCFYATITTELEPHHLSIAWMAQGVLEISWVAHEHCNHAFTSYMDND 170
DB      121 vvgvlstsslmwpvfswkyethrhentgslerdovfeykkhoelpmvtfyvytgmrvj 186
GY      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      121 TVGLTRCHLLDYTFECHKVCCHMCHMLCOLLAELEFECEKHFWKCG ENCLTERT 179
GY      187 whivvgltlmpvjlatnasrfpyet-lachtlvypfyndetaaqlvsdygwasy 245
GY      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      180 VMLTVGSFLDMVLILANVGSGTIDDSRKCHNFRTTYNRERKLTLTSADALAVGC 239
DB      245 IYKLAAGVGMVVVTWVYAPPLIENAKVIYVIGTHPSLPHYDSQEWDLTGALAMD 305
GY      240 LFRFAAGVMAVMVTVLVLLSN FHLITSLDGNSTSLPHTSCIMPFRRALATVE 299
DB      306 rldyglntvfnmtldtvahhlstimpylhametkallpiqdyhhldptpvakatre 365
GY      300 RDYGLINRFHNITDPGRAHNHCSMNPYHSBKAFAIKRTLDLYQGDFGCRVVFAMWAF 259
DB      366 aqeilyepe---dkgyfwynkl 387
GY      360 AKETIVPEEDPGEEKSVFTNNKL 364

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ID	RESULT	6
1D	R53702 standard; Proteolip, 387 AA.	
AC	R53702?	
PT	09-MAY-1994 (first entry)	
DE	Sequence of cDNA from <i>Heliothis virescens</i> Delta 12 desaturase derived from the cDNA	
DE	in plasmid pRFL97C-42.	
FM	Fatty acid desaturase, lipid unsaturated, transgenic plant.	
OS	<i>Gossypium commutatum</i> .	
PN	M0941516-A.	
PP	26-MAY-1994.	
PF	15-OCT-1993; 009987.	
PR	17-MAY-1992; 95-97339.	
PA	(GPO) ON POINT DE MEMOIRS 6 CO E I.	
P1	14-APR-94, Okady 30?	
DR	MT1: 94 18315/22.	
N	PCMB; G66073.	
PT	Genes for fatty acid desaturase enzymes - permit alteration of	
PT	plant lipid composition	
PC	Claim 12; Page 121, 133; 147pp; English.	
CV	A cDNA library made from a rat A-432 cell line from a developing	
CC	liver tumor (S-type IV, 20-25 MPA) was screened. Radio-labeled	
CC	liver tissue from a rat liver (S-type IV) was added and allowed to	
CC	hybridize. One of the strongly hybridizing plasmids and three of	
CC	the weakly hybridizing plasmids were purified. The inserts were	
CC	sequenced and the sequence of plasmid pRFL97C-42 is given in	
CC	G66073. An isolated cDNA and fragment were used to clone a cDNA	
CC	library in a cDNA library.	
CC	Isolate nucleic acid fragments encoding fatty acid desaturases	
CC	and related enzymes is claimed which comprises comparing AA	
CC	sequences in RFL97C-42 and other fatty acid desaturase sequences;	
CC	identifying conserved sequences of 4 or more AAs; designed degenerate	
CC	oligos based on the conserved sequences; and using the oligos to	
CC	isolate sequences encoding fatty acid desaturases and	
CC	desaturase related enzymes.	
SQ	Sequence 387 AA.	
Query Match	64.4%; Score 1466; DB 10; Length 387;	
Best Local Similarity	45.1%; Recd. No. 1,826-178;	
Matches	250; Conserved 59; Mismatches 71; Indels 5; Gaps 4;	
DB	1 mguymst.vt.usms.kaysheterphthkpyllglnhtrphcterststnt 60	
QY	1 M0941516-A V. STPS KCEITDTRVCEPPEYVOKAAIFHCKGKIPESYL 56	
DB	61 awnfctisysiatinfyispsisyawlywllqgcltqlwlnegchafsevg 120	
QY	57 IMDIILSRTAATTFEHLERSTAFELMAQVWVQVWVIAHCKHAFESQY 116	
DB	121 fddvqyltthaltayfswlyshstthhststlrdwvlykshlyssykyhmp 180	
QY	117 WIDWVQVLFVRLDLSWLSLHCHHCHHCHHCHHCHHCHHCHHCHHCHH 176	
DB	181 qvltlaarlllqplvlatnvegrpydr-lachydyppllseterlqlyadqlfat 239	
QY	177 GRTWVLLVQPLAMVLTIANNSSPFQCHHCHHCHHCHHCHHCHHCHHCHH 236	
DB	240 tlvlyqatmaklawnmlyqvplllvncflvmlylqthpralpryssewdllrgamv 299	
QY	237 TGLGKRKAAGVAMVCGVLLLVNCEVLVLTGHTTFSLFHTGSCDMEVRRALA 296	
DB	300 tvdrdyvylkvthnadihvahhlfatvphvhametkalprmpvyyrqrplykal 359	



















[illegible]

RESULT 15

1B R60499 standard; Protein; 446 AA  
 AC R60499;  
 DT 28-MAR-1995 (first entry)  
 DE linoletic-acid-desaturase fad6.  
 DE linoletic-acid-desaturase, fad6; transgenic plant; crop improvement;  
 KM linoletic acid.  
 OS Arabidopsis.  
 PN W09418337-A.  
 FD 18-AUG-1994.  
 FF 04-FEB-1994; U01321.  
 PR 05-FEB-1993; U5-014431.  
 PR 22-NOV-1993; U5-156551.  
 PA (MONS ) MONSANTO CO.  
 PA (UMMS ) UNIV MICHIGAN STATE.  
 PI Arctonid VnA, Gibson SJ, Kishore OM, Poff TG, Somerville CR;  
 DR WPI; 94-279758/74.  
 DR N-PSDB; Q71210.  
 PT Genetically transformed plants with altered linoletic acid  
 PT content - contg recombinant, double stranded DNA encoding  
 PT linoletic acid desaturase, or the antisense of the coding  
 PT sequence  
 PS Distosure; Page 75-77; 144pp; English.  
 CC The cDNA sequence and deduced amino acid sequence of linoletic-  
 CC acid-desaturase fad6 of Arabidopsis are provided  
 Sequence 446 AA;  
 SU

Query Match	22.13;	Score 664;	DB 11;	Length 446;
Best Local Similarity	37.44;	Prod. No. 1.25e 51;		
Matches	107;	Conserved 1107;	Indels 207;	Gaps 14;

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Db      81 eedkqkfdqgppppididataphwvkwmpkpslysvvdaav--falaagay 177
        | : | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      17 ETDNRKV--FCEPEFVCELSAIPFPHFNKSHRSSTLMDIILASCTYMAITFP 75
        | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      138 -l-n--nwlpvlylwgltmkulvlgldgqgaglsndpknswvhlhsstlyph 193
        | : : | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      76 LHPRLSTFAMPLTAAWAGQVLTGAWVTAECCHHAFSTQWLTDLVHFSRLTFP 135
        | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      194 gwisrtthqthqthqthqthqthqthqthqthqthqthqthqthqthqthqth 248
        | : | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      136 SWNSHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHHCHH 194
        | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db      243 waispjk--kys--lyhdsdillfphdldvlylswawamallvholfigpml 303
        | : | : | | | | | | | | | | | | | | | | | | | | | | |
Qy      195 AFNSRREYDGGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGHGH 254
        | : | : | | | | | | | | | | | | | | | | | | | | | | |
Db      304 lyagfpwlnwmlafvlylhhghqsklpwvqk--swylygltl--ldvylloahbi 362
        | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      255 FYCHLHNGSTLYHLYYGH THS LTHGCGGCMRFGCALVGHBDVLIAGNTH 312
        | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      364 -gftholhlfqfplvlylwaatvavpvtlkyvy 346
        | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      313 TDTHVAHHFSTHMHVNAEAKAKRLDLETYQ 346

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Submitted and published with the following references:  
 1. *Journal of the American Medical Association*, 291:1997, 1999.  
 2. *Journal of the American Medical Association*, 291:1997, 1999.











P1 Breun P91 Somerville, C., Van De Loo, Ely,  
 DR MPI, 96-20094/20.  
 N-PSDB, 172011.  
 PT Fruits of hydroxylated fatty acids, e.g. ricinoleic acid, hydrogenated  
 PT acid - in genetically modified plants such as rapeseed, flax,  
 PT sunflower, cottonseed, a fatty acid hydroxylase gene  
 PS Claim 17, Page 68-69, 165879, English.  
 PS A kappa fatty acid hydroxylase (kphx) is encoded by a cDNA clone  
 pKphxHyd (172901) isolated from a genomic library of *Brassica napus*  
 CC tendrils. The enzyme introduced a hydroxyl group 3 carbons distal  
 CC from a double bond located near the center of the fatty chain of  
 CC a fatty acid. It shows 92.2% similarity and 94.8% identity to  
 CC the Arabidopsis fad2 desaturase. Transgenic plants, esp. oilseed  
 CC plants, expressing pKphxHyd contain altered levels of hydroxylated  
 CC fatty acids, e.g., linolenic acid (18-hydroxy-11-tetrasenoic acid),  
 CC in seed oils, waxes and related products.  
 Sequence 384 Aa,

Query Match	87.0%	Score 9483	28 17	Length 384
Best Local Similarity	88.0%	Field No. 6.20E 325		
Matches	308	Conservative	41	Mismatches 347
			Indels 2	Gaps 27

[illegible]

RESULT	4
ID	R5364 standard; Prolinap 679 AA.
AC	R53699.
DT	09-NOV-1994 (first entry)
DE	Sequence of soybean microsomal delta-5 desaturase deduced from cDNA in
DE	plasmid pSF7-1698.
KW	Fatty acid; desaturase; lipid; unsaturated; transgenic plant.
OS	Glycine max.
PN	W09411516-A.
PD	26 MAY 1994.
PF	15-OCT-1993; 009987.
PR	17-NOV-1992; 05 977339.
TA	(DUF0 ) DU POINT DE NEMOURS & Co F.I.

P1 Lightner JP, Okuley JJ;  
WRJ; 94 1875/572.  
N-PSDB; Q66070.  
PT Genes for fatty acid desaturases: genetic alteration of  
plant lipid composition  
P6 Claim 13 Page 100 179; 14pp English.  
The gene responsible for Q66070 was identified by screening lambda phage  
cDNA library made with fatty Ac cDNA from developing apple seeds  
with radiolabeled probe. The cloned gene derived from  
Apple 129K, designated pA129K, was sequenced and determined plasmaid  
129K 129K was identical to one other is 129K with the Apple and Pear  
 accession number AF04 6007. An isolated nucleic acid fragment  
wherein the nucleic acid identity is 90% or greater to  
Q66070 is claimed. A method to isolate nucleic acid fragments  
encoding fatty acid desaturases and related enzymes is claimed  
which comprises comparing AA sequences in PDB1, PDB2 and other  
fatty acid desaturase sequences; identifying conserved sequences of  
4 or more AAs; designed degenerate oligos based on the conserved  
sequences and using the oligos to identify sequences encoding fatty  
acid desaturases and desaturase related enzymes  
Sequence 379 AA;

Nancy Math 64.68; 2006 21.87; CR 10; Length 270g  
 Post Local Similarity 70.58; Prod No 2 290-191;  
 W. locs 70.67; 2006 21.87; 2006 21.87; 2006 21.87

[illegible]

ACETIT 5  
 ID R53700 standard; Protein 387 AA.  
 AC R53700;  
 DT 09-NOV-1994 (first entry)  
 DE Synthesis of  $\alpha$ -methylcrotonyl-CoA-12-desaturase-deficient from the  
 PE cDNA in plasmid pBad2.1.  
 KW Fatty acid; desaturase; lipid; unsaturated; transgenic plant.  
 OS Zea mays.  
 RN M09411516-A.











RESULT	9
ID	R61498 standard; Protein, 283 AA.
AD	R60498;
DJ	28-MAR-1995 (first entry)
DE	linoleic-acid-desaturase fad3.
KW	linoleic acid desaturase fad3; oilseed rape; napus-seed;
KW	transgenic plant; crop improvement; first identified chromosome;
KW	VAC1 linolenic acid.
OS	Rutacea napae.
FN	M09418337-A.
SD	14-Aug-1994
RF	04-FEB-1994; 001321.
FR	05-FEB-1993; 05 014431.
FR	22-NOV-1993; 05-156551.
PA	(MOMS ) MORGANTO CO.
PA	(CHMS ) UNIV MICHIGAN STATE.
P1	Arendel VDA, Gibson SL, Rabinow CM, Boff TO, Somerville CR,
DR	WP1; 94-279758/34.
DR	N-ESTD; 071203.
PT	Genetically transformed plants with altered linolenic acid
PT	content - coding technology, J. Albert et al. DNA cloning
PT	linoleic acid desaturase of the absence of the coding
PT	sequence
PS	Disclosure; Page 69-70; 14ppp English.
CC	CNR encoding the linoleic acid desaturase (fad3) of B. napae was
CC	isolated from a YAC library using BEP 209 and AAC2 markers as
CC	probes. Isolated DNA was amplified using the primers given in
CC	Q71204 09, and used to screen TCR libraries. The fad3 gene was
CC	identified in PAC EMBL11.
CC	Sequence 383 bps.
Query Match	25.78% Score 779; EN 11; Length 383;
Best Local Similarity	40.06% Eval: MS: 6480 61;
Matches	133; Conservative 70; Mismatches 100; Indels 23; Gaps 16;
Dj	25 fgaagfklgltatgphkhwkepltemprldeavala mavyf d sst 77
Qy	1 11 :111 11 11 1 111 111 : : 11 11
25	fctcttvtvtefatatgttttttttttttttttttttttttttttttttttttttttt
Dj	78 lwplywaqqlfwalfvdhdqfnssdrlhswwghllsllypgnwlshth 137
Qy	1111 11 : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	85 amplymaccocvlwawlmhcchmawmewmleewlleflerellayfsmrshpna 144
Dj	138 hqhghvndeswrpl--pe kly-knlgs tmltyvylpml ypyilywyrspt -- 190
Qy	1 1 1 1 1 1 1 1 : : 1 1 1 1 1 1 1 1 : : 1 1 1 1 1 1 1 1
Qy	14 hmcngclereevtketrtkmzktldglrdrtwvact lmwtlatfvscvry 203
Dj	191 egr-s-hfypsslfpserklafstcwfmalatvyslfvdcvnykw-ygyrry 246
Qy	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	204 gcyhachmhmrntfrcehkrvynlmg tlavyyvymavgvam-wftcvlll 262
Dj	247 fwmldavetyllhhghdxeklpwrgbwswylrtalcdygnimtbl-griwhh 305
Qy	1 : : : : 1 1 1 : : 1111111111111111111111111111111111
Qy	263 vsgelvlltthr thnc lhmccgmwmkcalavgcvtollharynnrtttvahn 356
Dj	306 lpgtphyllvdatrakhlvgrry 331
Qy	11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy	321 lfslmehyamlaahkahtlnrdty 346
RESULT	10
ID	R37596 standard; Protein, 453 AA.
AD	R37596;

Dec 17 11:09

DT	01-OCT-1993	1st entry
EM	Genotype of soybean plasmid delta-15 dehydratase.	
EE	Inf-3 gene, 1993 - 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660	



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Db      379  LPPPIPhyhlwvctcldgprvqkyr 404
      11: :1111 :1111 11..11:
QY      321  LFTSMHYHAMEATKAIKPILEYYQ 346

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## RESULT 11

1D	R37591; Standard; Protein; 378 AA.
1E	R37591;
1F	01-06T-1993 (first entry)
1G	Sequence of microsomal delta-5 hydroxylipid desaturase.
1H	Island cosmids, <i>Acidithiobacillus</i> strain 211 desaturase cDNA.
1I	<i>Brassica napus</i> , clone pRNS3712.
1J	W09311245-AA.
1K	10 JUN-1993.
1L	03-DEC-1992; 010294.
1M	04-DEC-1991; 05-NOV-1994
1N	(DDBP) ) DDT PONT DE NEUMONS & ON E.L.
1O	Brownlee J, Gnan LP, Kennedy AJ, Brownlee DM, Wierzbicki AM, Yadav NS;
1P	WPL; 93-19/063/24.
1Q	N-PSDB; 043205.
1R	Isolated nucleic acid treatment, for plant lipid compsn.
1S	PT modification - comprises nucleic acid sequence encoding fatty
1T	acid desaturase or related enzyme with high amino acid identity to
1U	specific polypeptide
1V	Disclosures: Page 154-156; 105FF; Finnish.
1W	0.6kb was isolated from a cDNA library using a 5.2 kb Hind III
1X	fragment containing wild type gene. 30A as a full-length
1Y	hybridization probe. One of the sequencing primers made to the cDNA
1Z	insert was also used. The identity of the expression product of cDNA
2A	as the <i>Arabidopsis</i> cDNA. Both the proteinase was confirmed by
2B	the <i>Arabidopsis</i> cDNA expression in plant tissues. Isolated regions of
2C	R37592 are useful in designing long oligomers for hybridization as
2D	well as shorter ones for use as primers in the PCR. The sequences
2E	of useful regions are given in G33213 G42254. The cDNA inserts
2F	from pRT1 and pRTM were used to isolate cDNAs from <i>Brassica napus</i> 2
2G	was deposited as At00106.06055, pRNS373 (G42266) corresp. to a
2H	novel <i>Brassica napus</i> seed desaturase different from that shown in
2I	G43205.
2J	Sequence 378 AA;

Query Match:	93.34	Score 106; Pos 7; Length 379;
Best local Similarity	37.28;	Pred. No. 2736 54;
Matches	126; Conservative	61; Mismatches 113; Indels 19; Gaps 10;

[illegible][illegible]

## REFS1117 12

ID R3759b standard; Protein, 380 AA.  
 AC R3759b.  
 CF m1-m7-1993 (first entry)  
 CC Sequence of recombinant poly(1,3-sn-*phosphatidyl*  
 KM lipid composition modification, fatty acid desaturase, enzyme.  
 OS Glycine max, clone pXf1.  
 PN M09411245-A.  
 PB 10-JUN-1993.  
 UF 03-10-1997; 010564.  
 FA (R006) D9 F00T IE NLM0R5 & CO E 1.  
 PI Rousey J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,  
 PI Yadav NS.  
 DR WP17-93-197063/24.  
 FT Isolated nucleic acid fragment, for plant lipid composi-  
 FT tion. The sequence codes for a fatty acid sequence encoding fatty  
 FT acid desaturase or related enzyme with high amino acid identity to  
 FT specific polypeptide.  
 FT Enslinbauer, Eyrar 144 1446 16384, English.  
 E5 GPR was isolated from a cDNA library using a 5' to 3' Hind III  
 CC fragment containing wild type genomic DNA as a radiolabeled  
 CC hybridization probe. One of the sequenced fragments gave to the pGR3  
 CC insert was also used. The identity of the expression product of pGR3  
 CC as the Arabidopsis gene was confirmed by sequencing and confirmed by  
 CC its biological overexpression in plant tissues. Conserved regions of  
 CC fatty acid synthase and elongation factors for hydrolysis as  
 CC well as shorter ones for use as primers for the PCR. The sequences  
 CC of two full regions are given in G35613 G35624. Arabidopsis delta-15  
 CC desaturase cDNA was used as a hybridization probe to isolate a  
 CC glycerolipid desaturase cDNA from soybean. Inserted pXf1 was  
 CC deposited under ATCC 68874.  
 CC Sequence 380 AA;

Copy Match	23.3%	Score 70%	PR 7	Length 280
Best Local Similarity	29.6%	Prod. No. 340e54		
Matches 129	Conservation	74	Mismatch 100	Ratio 0.3
				Caps 197

[illegible]























































[illegible]

Search completed: Wed Dec 17 17:22:15 1997  
Job time : 1105 secs.







CC 06b06 is claimed. A method to isolate nucleic acid fragments  
CC encoding fatty acid desaturase and related enzymes is claimed  
CC which comprises: amplifying AA sequences in prokaryotic and eucaryotic  
CC fatty acid desaturase sequences; identifying conserved sequences of  
CC 4 or 6 nt AA; designing oligonucleotide probes based on the identified  
CC sequences; and using the probes to select sequences encoding fatty  
CC acid desaturases and desaturase related enzymes.  
CC Sequence 385 AA.

Query Match	90.56%	100% identity	16	16	100%	100%	
Best Local Similarity	92.48%	100% identity	16	16	100%	100%	
Matches	355	Conservative	7	Mismatches	21	Gaps	17

Db	1	mgagimgaypskkskdshkspoodpittvgekkakgphokkrspstshhadi	60
yy	1	MGAGGMGAYPSKKSCHSHKSPDPTTVEKKAGPHOKKRSPSTSHHADI	60
Db	61	hjascfyvattvfpjlpmpisylawp wacqgcvtlqgwvlahcqaafsdqwd	120
yy	61	HJASCFYATTVEFPJLPMPISYLAWP WACQGCVTLQGWVLAHCAAFSDQWD	120
Db	121	lvgljllhslllvpyfswkyshrhshcsglrcdevipr-sqtssglststlqtlv	179
yy	121	LVGLJLLHSLLVPHYFSWKYSHRHSHCSGLRCDEVIPR-SQTSGLSTSTLQTLV	180
Db	180	mltwgtltlmplylatfivsgdygdacthprapayndrelqylsdsagllavcy	239
yy	181	MLTWGTLTLMPLYLATFIVSGDYGDACTHPRAPAYNDRELQYLSDSAGLLAVCY	240
Db	240	lpjyavqgfrasmwvcllmpjlltwgglvllvtyqstprspbydseswddkryajlatvdi	299
yy	241	LPJYAVQGWASMWVCLLMPJLLTWGGVLVLTYSQSTPRSPBYDSSEWDDKRYAJLATVDI	300
Db	300	dyajlloglthlathhahllstmplyhamaykalkpjllyagvfgqtpvokamkrvg	359
yy	301	DYAJLLOGLTHLATHHALLSTMPLYHAMAYKALKPJLYAGVFGQTPVOKAMKRVG	360
Db	360	kcclyvepdrqpekkyvlwywkl	383
yy	361	KCCLYVEPDRQEKKCVLWYWNKL	384

RESULT 2

ID R53697 standard; Protein; 363 AA.

Ac R53697;

DE 09-NOV-1994 (first entry)

DE Sequence of mitochondrial 3'-12' deoxyribose,

KM Fatty acid; deoxyribose; lipid; unsaturated; transgenic plant.

OS Arabidopsis thaliana.

PN M09411516-A.

PD 26-MAY-1994.

PR 15-OCT-1993; 009967.

PR 17-NOV-1992; 08-977314

PA (DDBP) DE FRONT DE NEMOIRS 5 68 E. I.

P1 Lightner JE; Okuley JJ;

DR WP1; 94-183515/22.

DR N-FSDB; Q66068.

FT Genes for fatty acid dehydrogenase enzyme protein alteration of

FT plant lipid composition

PS Claim 13; Page 112-114; 147pp; English.

OC The gene *acfat-1* (Q66068) was cloned by screening A. thaliana

CC genomic DNA library using radiolabeled pGEM2cDNA insert, purifying

CC positively-hybridising plaques, and subcloning a 6Kb Hind III insert

CC fragment from the phage DNA in pBluescript vector. Comparison of the

sequence of the gene (G66074) revealed the presence of a single initiation of 114 bp, between the sequences 5' and 3' of the gene, which is a particularity for the initiation of a protein. A motif, 12 bp of nucleotides, 5' of the initiation site, is found in all the sequences of the gene. This motif is a particularity of the gene, which is unique among all the sequences of protein domain and other fatty acid desaturase polypeptide sequences. Identifying conserved sequences of 1 or more AATs displaying domains in all the conserved sequences and using the degenerate oligos to isolate sequences encoding fatty acid desaturases of reduced enzymes.

Query Match	90.3%;	Score 2735;	DP 10;	Length 383;
Best Local Similarity	89.3%;	Pred. No. 3748	253;	
Matches	343;	Conservative	19;	Indels 1;
				Gaps 1;

[illegible]

RESULT	3
ID	P95579 standard; Protein; 384 AA.
AC	P95579.
DT	10-SEP-1996 (first entry)
DE	Kappa fatty acid hydroxylase, <i>Lesquerella</i>
KM	Kappa fatty acid hydroxylase, <i>Lesquerella</i> plant;
KW	aliphatic acid 1-oxidase; Cramer; Brassica family; crucif; alkyl
KW	enolase; squalene; oxidase; cyclo-oxygenase; cyclooxygenase; coenzyme
KW	oil palm; corn.
OS	<i>Lesquerella fendleri</i> .
PN	W09610075-A1.
PD	04-APR-1996.
PE	26-SEP-1995; 011855.
PR	26-SEP-1994; US-516596.
PP	11-OCT-1994; US-5120982.
PP	26-SEP-1995; US-520092.
PA	(BROU) BROU P.
PA	(SWE) SOMPELLE C
PA	(VIAO) VAN DE LIND F J.







PB	26-MAY-1994.
PF	15-OCT-1993; D09987.
PR	17-NOV-1992; US-971339.
FA	(DDBJ) GenBank Entry No. F01339.
PI	Lighthouse JE, Okamoto JI,
OR	MPLJ 94-183615/22.
DR	NFSEBj_056071.
PT	Genes for fatty acid desaturase enzymes - genetic alteration of plant lipid composition
FC	Corn microsomal delta-12 desaturase cDNA was isolated using a PCR approach. A cDNA library was made to poly A+ mRNA from developing corn embryos. This library was used as template for PCR using sets of degenerate oligos NS1 (G66074) and PMSA/RH (G66077,G66078) as sense and antisense primers, respectively. NS3 and PRSA/RH correspond to stretches of AAG 104-109 and GAA-336, respectively, of R53497, which are conserved in most microsomal delta-12 desaturases. A PCR product of 720bp was purified and used as a probe for screening the cDNA library. A single was purified and found to encode microsomal delta-12 desaturase truncated at the 3' end. This cDNA was used to probe the corn cDNA library again. The clone con- firmed the longest insert, designated Pfad1, was sequenced completely (G66077). An isolated nucleic acid fragment wherein the nucleic acid identity is any or greater than about G66077 is claimed. A method to isolate nucleic acid fragments encoding fatty acid desaturase and related enzymes is claimed. Which comprises comparing AA sequences to G66047 p9309 and other fatty acid desaturase sequences, identifying conserved regions, if it or more Aas designed dependent probes based on the conserved sequences; and using the oligos to isolated sequences encoding fatty acid desaturases and desaturase related enzymes.
SQ	Sequence 387 Aat
Summary Match:	69,73% Score 2289, bit 13 Length 387
Boot Local Similarity:	69,15% Prob: N=1440 M=7
Matches 266;	Conservative 46; Mutated-bps 69; Indels % Gaps %
Ddb	7 mlekereckqsqaratltygaamqtspvokprftlgakkaipnroforssketyvhol 66
Gy	1 MACGGMGYSPFSKKELETHREHYLTSTFTTGELTAAIHDFEGRSFPSLTLMT 60
Ddb	67 viaaaillfalaiipalpslltlyaaamlpyiaagvwctgwawiahocghafsyasl 176
Gy	61 IASCFYVAATTPFLPRLPHLSYEAMFLYAQCWAVTCGWAWIAHCQHAFSDYCWM 120
Ddb	127 vvgqltlhsasmrpfyskyshrtstntgslerdevfpkkkeallpwtfpyvmypgr 186
Gy	121 TPCILRCELGLTYECMWYGHSHNHNVTGCHITETVFTRERCRITKWYALINPKRT 179
Ddb	187 thivavqltlgwpdyltasngsfyyer-facilfdrypiyndnraqiatsdyavaalg 245
Gy	189 WMLTVPGTLMWLVLADNVGSNGHTYSBDAHLHHRAFLTYNRERRDYITSNSGIATAVG 239
Ddb	246 lyklaaatgvwvvuvayavltnawvlitleyiqhtpslphidssewdwlrgalatmd 305
Gy	246 LPAANACGVAAVMVEFYCVGLTIIVATLVALLTLGNTEGLEHNPDESCWTARALATVD 299
Ddb	306 fdglvnlrvthmtclthvahhlstmphyameakaikarpdgdyhfcprvakatwe 365
Gy	300 KDTGLLNKNVNNHIIIDTNAAHLSTMPRYTAAMAATKAIRPLDSGYQLHGPPVKAAAME 359
Ddb	366 agecgyvepe--di-kaviwyalki 387
Gy	360 AKKCIYVERLDUGGERKKVFWTKNL 364

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RESULT 6
1c K03022.2 Arabid, F1:Arab, 387 AA.
2c R30302.
3c 09 NOV 1994 (first entry)
DE Sequence of cation microsomeal delta-12 desaturase deduced from the cDNA
4c in Phaseol F8197-42.
5c
6c Fatty acid, desaturase, lipid, unsaturated, lysozyme plant.
7c
8c
9c
10c
11c R09411516-A.
12c
13c 26-MAY-1994.
14c
15c 15-NOV-1993; 000487.
16c
17c 17 NOV-1992; US-971339.
18c
19c 1990- ) 001987 OF MEMBERS 6 CO E L.
20c
21c Lighter 09, Okaley 007
22c
23c MFI: 94-18315/22.
24c
25c N-PSDB: 066073.
26c
27c Desat-12 fatty acid desaturase, enzyme, plant, structure of
28c plant lipid composition
29c
30c Claim 13; Page 131-133; 147pp; English.
31c
32c A cDNA library made to poly A+ mRNA isolated from developing
33c castor beans (stage IV, 20-25 DAF) was screened. Radio-labeled
34c probes (106 cpm) of cDNA of F8197-42 were added and allowed to
35c hybridize. Three of the strongly hybridizing clones and three of
36c the weakly hybridizing clones were purified. The genes were
37c sequenced and the sequence of Phaseol protein 42 is given in
38c Genbank. At least one nucleotide difference between the nucleotide
39c identity is 99.4 percent. A sequence of 2667 nt. A motif of
40c acyl-acyl-acyl and hydroxyl-acyl-acyl fatty acid desaturases
41c and related enzymes is shared with a different desaturase AA
42c sequences in p14697 R3707 and other fatty acid desaturase sequences;
43c identifying conserved sequences of 4 or more AAs; desaturase domain
44c motifs based on the conserved sequences; and using the motifs to
45c identify sequences encoding fatty acid desaturase and
46c desaturase-related enzymes.
47c
48c Sequence 387 AA;
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QY 291 TWBNCSTIMVBNITDTHVANHLS'DMHHAMKATRAINPLISGYVQJACTVVRAM 386  
 Db 360 weakelivepde-gartqytwyeh 386  
 |||||||:||||:|||||  
 QY 357 WREAKECTIVEPDRQENGVHWNK 383

RESULT 7  
 ID R33701 standard; Protein; 224 AA.  
 AC R33701;  
 DT 09-NOV-1994 (first entry)  
 DE Sequence of castor microsomal delta-12 desaturase deduced by the cDNA  
 KM in plasmid pRF2-1C.  
 NM Fatty acid; desaturase; lipid; unsaturated; transgenic plant.  
 OS Ricinus communis.  
 PN M09411516-A.  
 PE 26 MAY-1994.  
 PF 15-OCT-1993; 009481.  
 PR 17-NOV-1992; US-917334.  
 RA (DDPG.) DU PONT DE NEMOURS & CO E. I.  
 PI Lightner JE, Okuley JJ.  
 DR WPI1\_94-183515/22.  
 NR N-PSDB; 066072.  
 PT Genes for fatty acid desaturase enzymes - permit alteration of  
 PT plant lipid composition.  
 FT Claim 13; Page 129; 147pp English.  
 CC Polysomal mRNA was isolated from root beans of stages 1-11 (0  
 CC 10 DAF) and also from castor beans of stages IV-V (20-25 DAF).  
 CC 10 ng of each mRNA was used for separate RT-PCR reactions.  
 CC The reverse transcriptase reaction was primed with random  
 CC hexamers and the PCR reaction with sequence delta-12  
 CC desaturase primers NS1 and NS2 (Gutierrez, 1990b). A cDNA fragment  
 CC of approx. 700 bp was amplified from both stage 1-11 and stage  
 CC IV-V mRNA. The amplified DNA fragment was ligated into a vector  
 CC was gel purified and cloned into a vector to create plasmid  
 CC pRF2-1C. The 700 bp insert in pRF2-1C was sequenced (066072).  
 CC An isolated nucleic acid fragment wherein the nucleic acid identity  
 CC is 90% or greater to sequence 066072 is claimed. A method to  
 CC isolate nucleic acid fragments encoding fatty acid desaturases  
 CC and related enzymes is claimed which comprises: comparing AA  
 CC sequences in pRF2-1C and "test" fatty acid desaturase sequences;  
 CC identifying conserved sequences of 4 or more AAs; designing degenerate  
 CC oligos based on the conserved sequences; and using the oligos to  
 CC isolate sequences encoding fatty acid desaturases and  
 CC desaturase-related enzymes.  
 SQ Sequence 224 AA;

Query Match 46.6%, Score 1479, DR 19%, Length 224;  
 Best local similarity 79.6%, Field No. 1176 129;  
 Matches 180; Conservative 24; Mismatches 29; Indels 2; Gaps 2;

Db 1 wmahdeghafdsyqlldvuyllhscllvpyfswkshtrhshpysgldevyvk 60  
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 QY 101 WVIHNVCHHAFSTYQIMVTCVTFHSEIVTFESWYSHRSHNSCTSLREVEVPE 160  
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 Db 61 kksaiwskylnnpqfmlavtllsllwpylalfvnsqrpydt-fachydpqpyind 119  
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 QY 161 EKESITWYKALNGLSHFTWMTVATLFWKELAAEVSGRGRVACAFHFRNATFTR 220  
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 Db 120 terlefiedaylavtfglyglakqlawvovypylvovsflvlltllqthpal 179  
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 QY 221 PERGQIVTCASIALATVYDHFALAAVQVAMWTFVSCCLVYDFVLTLLASHTGSS 260  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 180 phdsewmdlrgalatavtdyglhkvhultdtgyahll-temp 224

QY 281 FHEECSTWMLBATALVGRVYSLHFRVNTITDTHVANHLS'PSTWMD 226  
 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 116 plmblayryl-cytsprk-eg--s-hloryestlsfreskll-astvswsinfvela 229  
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 QY 185 QFT-LDMPLVLAIVNSGRVYDGRACNHRNAPYNDNRHLDQVITSDACILAVCY GIVR 242  
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 Db 230 lsfvgrplavlkvyvryaltlvmldavtllhhbrdcklmyrkykewylrgglitid 289  
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 QY 242 YAMQVAMKMGVGVYVPLVNGSEIVLTIVQGH TIPS LHRYSSEPMWMLRRLATVVR 300  
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 Db 290 dygltfmlhndt-ghvllhllpqlrphvhlvdakkaakvlguyt 324  
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 QY 301 DYGLDKVYHNTIDTHVANHLS'DMHHAMKATRAINPLISGYVQJACTVVRAM 386  
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RESULT 6  
 ID R33792 standard; Protein; 386 AA.  
 AC R33792;  
 DT 01 OCT-1993 (first entry)  
 DE Sequence of delta-15 desaturase.  
 KM Lipid composition; modification; fatty acid desaturase; enzyme.  
 OS Arabidopsis thaliana; clone pRF3.  
 PN M09311245-A.  
 PE 10-JUN-1993.  
 PF 03 DEC-1992; 010284.  
 PR 04 DEC-1991; US-804299.  
 RA (DDPG.) DU PONT DE NEMOURS & CO E. I.  
 PI Brown J, Gray LD, Kinney AJ, Pierce JM, Mierzbicki AM,  
 PI Yachiv NS.  
 DR M-PSDB; 043202.  
 PF 15-OCT-1993; 009481.  
 PT Isolated nucleic acid fragment, for plant lipid composi-  
 PT modification - compares nucleic acid sequence encoding fatty  
 PT acid desaturase or related enzyme with high amino acid identity to  
 PT specific polypeptide.  
 FT Claim 13; Page 127 129; 167pp English.  
 CC pRF3 was isolated from a cDNA library using a 5' to Hind III  
 CC fragment and cloned with "type" primer RNA as a template.  
 CC hybridization probe one of the sequencing primers made for the pRF3  
 CC insert was also used. The identity of the expressed product of pRF3  
 CC as the Arabidopsis delta-15 desaturase was confirmed by  
 CC 15 kDa apparent molecular weight in plant tissues. Conserved regions of  
 CC pRF3 are used in designing long oligomers for hybridization as  
 CC well as short probes for use as primers in the PCR. The sequences  
 CC of useful regions are given in 043202 043204  
 SQ Sequence 386 AA;

Query Match 26.0%, Score 787, DR 7%, Length 386;  
 Best local similarity 39.6%, Field No. 3 876 62;  
 Matches 123; Conservative 74; Mismatches 111; Indels 24; Gaps 18;

Db 6 lmgvthpghhkhvthfdeagctfhtfghfhwkftfscvuyvhlava 67  
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 QY 6 FMVCHSHMDELDHNV FENFTFVCHHAAVHFRSHCHFRCHVLDGGLAG 64  
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 Db 68 ala ladvr v d swtlwryuagzllfmltfvrdofygsfdrllnswvph 120  
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 QY 69 CEYVATFEPRLNPLSEFMDLWMAQCIVLGVVAVARQGNHAFQVMDITVOL 124  
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 Db 121 lksstlpryugvkhbthbthfctcdewrpfet v ykk ltho ttmlylv 175  
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 QY 125 FHEECSTWMLBATALVGRVYSLHFRVNTITDTHVANHLS'PSTWMD 184  
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 Db 116 plmblayryl-cytsprk-eg--s-hloryestlsfreskll-astvswsinfvela 229  
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 QY 185 QFT-LDMPLVLAIVNSGRVYDGRACNHRNAPYNDNRHLDQVITSDACILAVCY GIVR 242  
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 Db 230 lsfvgrplavlkvyvryaltlvmldavtllhhbrdcklmyrkykewylrgglitid 289  
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 QY 242 YAMQVAMKMGVGVYVPLVNGSEIVLTIVQGH TIPS LHRYSSEPMWMLRRLATVVR 300  
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 QY 301 DYGLDKVYHNTIDTHVANHLS'DMHHAMKATRAINPLISGYVQJACTVVRAM 386  
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RESULT 9  
 ID R60499; accession: 11; length: 363 AA.  
 AC R60499;  
 DT 28-MAR-1995 (first entry)  
 DE Lipoic acid desaturase (adt3).  
 KW Lipoic acid desaturase (adt3).  
 KW transgenic plant; crop improvement; yeast artificial chromosome;  
 KW YAC; lipoic acid.  
 OS Brassica napus.  
 PN W09418331-A.  
 PD 18-AUG-1994.  
 PF 04-FEB-1994; 001321.  
 PR 05-FEB-1993; US-014431.  
 PR 22-MAY-1993; US-156551.  
 PA (MONS) MONSANTO CO.  
 PA (UNMS) UNIV MICHIGAN STATE.  
 PI Arandel VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR,  
 DR WP1; 94-279758/34.  
 DR N-PSDB; 021203.  
 PT Genetically transformed plants with altered lipoic acid  
 PT content - contg recombinant, double-stranded DNA encoding  
 PT lipoic acid desaturase, at the absence of the coding  
 PT sequence  
 PS Disclosure Page 63 72; 116pp; English.  
 CC cDNA encoding the lipoic acid desaturase (adt3) of B. napus was  
 CC isolated from a YAC library using pH1.139 and A2A2 markers as  
 CC probes. Isolated cDNA was amplified using the primers given in  
 CC Q12004-09, and used to screen YAC libraries. The Adt3 gene was  
 CC identified in YAC EW7611.  
 SQ Sequence 363 AA;  
 Query Match 23.3% Score 705; DB 7; Length 453;  
 Post local similarity 40.83; End 100; 100; 100;  
 Matches 128; Conservative 69; Mismatches 102; Indels 23; Gaps 19;  
 Db 78 lmplyaaagtlfwaivlgdhcphgtsdprllnsavghlshfllpyghmkisrth 137  
 QY 85 AMPLYAAAGGCVLVQWVLAHVGMAHSGVMAHSGVMAHSGVMAHSGVMAHSGV 134  
 Db 138 nqnhghvndeswpl--pe-kly knlpus tnmlyvprlmayrlywyspjk-- 190  
 QY 145 HSNSTGHEDEVEFFKKNKJLWCKELNNPDSKVMILVCF LKMLYLKFNVSDETF 203  
 Db 191 eg--s-hfpyssifapserllastcwfmlatlvlsitlvprvtvk--vyvyii 246  
 QY 204 GSGCAHCHGVAPLYNCHDEGLTISNAG LAAV KGLFYAAVGVAAVSWVYVDEII 262  
 Db 247 fwmldavtylhhghdeklpwyrkeweyiagtelch dyglfnahddi-qfwhh 305  
 QY 263 VNGCLVLTLYQH-THRS LHYGNSFWWIRGALATVPRVGLINVRINTDPHVAHQ 320  
 Db 306 lfpglphylvatrakvhlqvyt 331  
 QY 321 LFSTFHHAMATRAKINFLDEETQ 346  
 RESULT 10  
 ID R37596; accession: 11; length: 453 AA.  
 AC R37596;  
 DT 17-JUN-1993 (first entry)  
 DE Sequence of soybean plastid delta-15 desaturase.  
 KW delta-15 desaturase (delta-15 desaturase).  
 KW clype max; clone pcdp 118bp.  
 PN W09311245-A.  
 PD 10-JUN-1993.  
 PF 03 DEC 1992; 010284.  
 PR 04 DEC 1992; US R04750.  
 PA (DDBP) DU PONT DE NEMOURS & CO E.I.  
 PI Reverse J, Guan LP, Kinney AJ, Pierce JW, Winzbrock AM,  
 P1 Yadav NS.  
 DR WP1; 93-07063/24.  
 DR N-PSDB; 043708.  
 PT Isolated nucleic acid fragment, for plant lipid compn.  
 PT modification - compares nucleic acid sequence encoding fatty  
 PT acid desaturase or related enzyme with high amino acid identity to  
 PT specific polypeptide  
 PS Disclosure Page 148 150; 167pp; English.  
 CC pcdp3 was isolated from a cDNA library using a 5.2 kb Hind III  
 CC fragment containing wild-type genomic DNA as a radiolabeled  
 CC hybridization probe. One of the sequencing primers made to the pcdp3  
 CC insert was also used. The identity of the expression product of pcdp3  
 CC as the delta-15 desaturase was confirmed by sequencing the cDNA  
 CC its biological expression in plant tissues. Overlapped regions of  
 CC R3752 are useful in designing long oligonucleotide applications as  
 CC well as short ones for use as primers in the PCR. The sequences  
 CC of several regions are given in G43073 G43074. A delta-15  
 CC delta-15 desaturase cDNA was used as a hybridization probe to isolate a  
 CC cDNA encoding delta-15 desaturase from soybean. Plasmid pcdp1 was  
 CC delta-15 desaturase cDNA was used as a hybridization probe to isolate a  
 CC cDNA encoding delta-15 desaturase from soybean. The insert of  
 CC pcdp1 (18bp) encodes a stretch of 16th nucleotides which contained  
 CC an open reading frame encoding a polypeptide (87092) of about  
 CC 803 identity with, and consistent with, the Arabidopsis delta-15  
 CC delta-15 desaturase polypeptide listed in P23993. Nucleotides 149  
 CC to 382 encode the putative plastid pcdp3, which with  
 CC and sharing some homology with the transit peptide described for  
 CC the Arabidopsis plastid delta-15 desaturase (R37593).  
 SQ Sequence 453 AA;  
 Query Match 23.3% Score 705; DB 7; Length 453;  
 Post local similarity 41.03; End 100; 100; 100;  
 Matches 128; Conservative 73; Mismatches 102; Indels 23; Gaps 19;  
 Db 98 fgaafffnaditaaipkhwwkprwtmsyyvrvv-av tglvvaay--ln--nml 150  
 QY 25 PCETPPFVGEIKRAIPHCKRSIPRSFYLIMDIINAFYVATVFFLLDPLPSVF 84  
 Db 151 wvplyaaagtlmwaivlgdhcphgtsfmsklnsvghlshfllpyghmkisrth 210  
 QY 85 AMPLYAAAGGCVLVQWVLAHVGMAHSGVMAHSGVMAHSGVMAHSGVMAHSGV 134  
 Db 211 fphghaewdwkpl--pe-kly knlpus tnmlyvprlmayrlywyspjk-- 260  
 QY 145 HSNSTGHEDEVEFFKKNKJLWCKELNNPDSKVMILVCF LKMLYLKFNVSDETF 203  
 Db 263 fwmldavtylhhghdeklpwyrkeweyiagtelch dyglfnahddi-qfwhh 305  
 QY 321 LFSTFHHAMATRAKINFLDEETQ 346  
 Db 320 fwmldavtylhhghdeklpwyrkeweyiagtelch dyglfnahddi-qfwhh 378  
 QY 263 VNGCLVLTLYQH-THRS LHYGNSFWWIRGALATVPRVGLINVRINTDPHVAHQ 320



































Dec 17 14:18

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*/ds\_xref=pid:gq0450"*

"MILLETIUS SP. NOVAE ZEALANDIAE PRIMUM NOTUM  
IPHOCAULIS STYVITOLSPATRYATTETHELOPOSLAMPITANON, LAM-  
GVALIBUCHHAE SRYAWOVLIGLHLLIVE SWNLSRHHCHTOSIDDEVEY  
FVKRSVMAKSTYNLEIGHAVSIVHTICOMYLAPOSCHOTISAPXAY  
PIYSRPHLLIYSDVAFSVTSIKYAKILKOWLYOCYCPALLINCEADITIYI  
QTHHAPHDSIKWENESAKIMPCOTHLRTHTITIVNAHFTSMBRGA  
EALMLILITLTCTCSTHAMBREACTYACLESCLCVYVERFY"  
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POLYA SITE      373 a      332 c      306 g      442 t  
BASP COUNT      981038

[illegible]

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[illegible]

FEATURES	SOURCE	RESULT	6
NAME		9422376	1440 DP
DEFINITION		ribonuclease inhibitor 12 hydroxyacyl-CoA, complete cds.	14-001-1495
ACCESSION		9722308	
NID		q722350	
KEYWORDS			
SOURCE		eastern bean.	
ORGANISM		ribonuclease	
REFERENCE		Eukaryotic mitochondrial exoribases; Viridiplantae; Charophyceae; Euphytiophyta; Euphytiophyta; Magnoliopsida; Malvaceae; Euphorbiaceae; Ricinus. 1 (bases 1 to 1440)	
AUTHORS		van de Loo, F.J., Benda, F., Turek, S. and Somerville, C.	
TITLE		An epsilon 12 hydroxyacyl CoA ribonuclease homolog desaturase homolog	
JOURNAL		Plant. Mol. Appl. Sci. U.S.A. 92 (7), 4743-4747 (1995)	
MEDLINE		97350145	
REFERENCE		7 (bases 1 to 1440)	
AUTHORS		Somerville, C.R.	
TITLE		ribonuclease	
JOURNAL		Submitted (08 MAR 1995) Chris R. Somerville, Plant Biology, Carnegie Institution of Washington, 980 California Street, Stanford, CA 94305-4111, USA	
FEATURES		location/analysis	
SOURCE		1..1440	

[illegible]















[illegible][illegible]







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23

Query Match	2.9%;	Score 34;	DB 61;	Length 1622;
Best Local Similarity	64.2%;	Prod. No. 1.52e-07;		
Methods	77;	Conservation	0;	Winged Pins 41;
			Indels	0;
			Gaps	0;

[illegible]

Search completed: Wed Dec 17 14:19:05 1997  
Job time : 1659 secs.



(T1)

Release 210 John F. Collins, Recompiling Research Unit,  
Crim. Div. ( ) 1990, 1994, 1995, 1996, 1997, 1998, 1999,  
Distribution rights by Interlock, Inc.

MSearch on:  -  database search, using Smith-Waterman algorithm

Run on:  Wed Nov 17 14:59:37 1993, Modified time: 957.70 seconds

Tabular output not provided.

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      700000          890328572.027A.3
Description:    (1-115) f.f.m H099770000A.ssq
Perfect Score: 1154
N.A. Sequence: 1 ATGGTAAAGGAGAAAT.....GTGAAAGAGAGATAAAT 1168
               TACCAAGGAGACTGCTTA.....CAGGTCATTATTAAT
(Comp:

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Scoring table: TABLE default

March	STP	Edison	of	Copy	of
March	STP	Edison	of	Copy	of

Listing first 45 entries

Database:

18CT 2550 18CT 2550 18CT 2550 18CT 2550 18CT 2550  
90FT 2000 90FT 2000 90FT 2000 90FT 2000 90FT 2000  
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Database: 18CT 2550 18CT 2550 18CT 2550 18CT 2550 18CT 2550

[illegible][illegible]

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Database:
118:ROD_119:SN 120:GNA 121:PHI
0-emb150_99
122:part1

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Dec 17 15:26 /home/fuller/dec07/US-08-572-002A-3.rge

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	EB	ID	Description	Freq. No.
1	952	82.5	1381	60	BL005687	R. juncus mpa for cde	8,34e+00
2	811	79.3	1372	59	AF010266	Arctidopsis thaliana	0.00e+00
3	471	41.3	1654	6	U00006A	cytochrome cde 2 mt	0.00e+00
4	421	39.2	1472	67	U000010	cytochrome cde mpa 42	0.00e+00
5	352	38.5	1453	67	U000040	cytochrome cde mpa 40	0.00e+00
6	296	28.2	1440	64	U000238	cytochrome cde mpa 38	1.60e-02
7	121	10.5	1170	62	U000118	cytochrome cde mpa 18	4.60e-06
8	56	4.9	1515	61	D43688	wheat mpa for cde 25	2.40e-11
9	39	3.4	1366	68	U000583	tobacco leaf mpa for	2.40e-11
10	37	3.2	215	57	U00278	sequence 5' from cde	8.50e-10
11	37	3.2	1288	12	U00011	rice mpa for w 3 fat	8.50e-10
12	33	3.0	1398	6	U00011	rice mpa for w 3 fat	8.50e-10
13	33	2.9	1383	60	U000118	rice mpa for w 3 fat	8.50e-10
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## ALIGNMENTS

RESULTS	1	RNA	FLN
LOCUS	ROTDESAT	1381 bp	
DEFINITION	B. juncea mRNA for oleate desaturase.		







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111

polyA site	373 a	332 c	306 g	442 t
BASE COUNT				
ORIGIN				

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15

[illegible]

RESULT	+		
Isolate	F-7936	1440 bp	mRNA
DEFINITION	Rhizinus communis cleave 12 hydroxylase gene, complete cds.		
ACCESSION	G72378		
NID	9722350		
KEYWORDS	.		
SOURCE	Castor bean,		
ORGANISM	Rhizinus communis		

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 1440)	Van de Lee, P. J., Brown, P., Turner, C. and Somerville, C	An oleate 12-hydroxylase from <i>Ricinus communis</i> L. is a fatty acyl desaturase homolog	Proc. Natl. Acad. Sci. U.S.A.	92 (1995), 6143-6147 (1995)	2 (bases 1 to 1440)	Somerville, C. R.	Direct Submission	Submitted (08-MAR-1995) <i>Ricinus</i> R. Somerville, Plant Biology, University of California, 1 Shields Hall, 950 Shields Hall, University of California, CA 94305-4101, USA

FEATURES	location/Qualifiers
source	1, 1440 "Fictitious Communism" /strain "Baker 296"
CDS	411, 1000 "Avalanche of Communism" 187, 1350

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GLAVTGECHQHAASEVQLADDVGLIVSHALLVTFQWVTSRRHSINIGLEDE

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23

Query Match

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Best local Similarity 64.2%; Prod. No. 1.54e-07;

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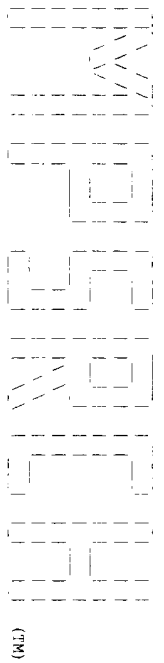
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Db 1141 cccacattatcatttgatagaaactactgaagctgctaaagccagtactgggaagtatta 1208

yy 975 GCTGCATTATACCCGATGCAAGCTTACCAACCCATATAAATTCATATCTTACAGAGTATTA 1034

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49: INVILL 46: PETA 47: NEWBL 48: ZANDRO 49: VANDI 50: VRIE 51: 52: VOTI 53: VATT 54: OGA 55: OGA 56: OGA 57: PATI 58: L

09:10:00 00:10:00 01:10:00 02:10:00 03:10:00 04:10:00 05:10:00 06:10:00 07:10:00 08:10:00 09:10:00 10:10:00 11:10:00 12:10:00 13:10:00 14:10:00 15:10:00 16:10:00 17:10:00 18:10:00 19:10:00 20:10:00 21:10:00 22:10:00 23:10:00 24:10:00 25:10:00 26:10:00 27:10:00 28:10:00 29:10:00 30:10:00 31:10:00 32:10:00 33:10:00 34:10:00 35:10:00 36:10:00 37:10:00 38:10:00 39:10:00 40:10:00 41:10:00 42:10:00 43:10:00 44:10:00 45:10:00 46:10:00 47:10:00 48:10:00 49:10:00 50:10:00 51:10:00 52:10:00 53:10:00 54:10:00 55:10:00 56:10:00 57:10:00 58:10:00 59:10:00 60:10:00 61:10:00 62:10:00 63:10:00 64:10:00 65:10:00 66:10:00 67:10:00 68:10:00 69:10:00 70:10:00 71:10:00 72:10:00 73:10:00 74:10:00 75:10:00 76:10:00 77:10:00 78:10:00 79:10:00 80:10:00 81:10:00 82:10:00 83:10:00 84:10:00 85:10:00 86:10:00 87:10:00 88:10:00 89:10:00 90:10:00 91:10:00 92:10:00 93:10:00 94:10:00 95:10:00 96:10:00 97:10:00 98:10:00 99:10:00 100:10:00 101:10:00 102:10:00 103:10:00 104:10:00 105:10:00 106:10:00 107:10:00 108:10:00 109:10:00 110:10:00 111:10:00 112:10:00 113:10:00 114:10:00 115:10:00 116:10:00 117:10:00 118:10:00 119:10:00 120:10:00 121:10:00 122:10:00 123:10:00 124:10:00 125:10:00 126:10:00 127:10:00 128:10:00 129:10:00 130:10:00 131:10:00 132:10:00 133:10:00 134:10:00 135:10:00 136:10:00 137:10:00 138:10:00 139:10:00 140:10:00 141:10:00 142:10:00 143:10:00 144:10:00 145:10:00 146:10:00 147:10:00 148:10:00 149:10:00 150:10:00 151:10:00 152:10:00 153:10:00 154:10:00 155:10:00 156:10:00 157:10:00 158:10:00 159:10:00 160:10:00 161:10:00 162:10:00 163:10:00 164:10:00 165:10:00 166:10:00 167:10:00 168:10:00 169:10:00 170:10:00 171:10:00 172:10:00 173:10:00 174:10:00 175:10:00 176:10:00 177:10:00 178:10:00 179:10:00 180:10:00 181:10:00 182:10:00 183:10:00 184:10:00 185:10:00 186:10:00 187:10:00 188:10:00 189:10:00 190:10:00 191:10:00 192:10:00 193:10:00 194:10:00 195:10:00 196:10:00 197:10:00 198:10:00 199:10:00 200:10:00 201:10:00 202:10:00 203:10:00 204:10:00 205:10:00 206:10:00 207:10:00 208:10:00 209:10:00 210:10:00 211:10:00 212:10:00 213:10:00 214:10:00 215:10:00 216:10:00 217:10:00 218:10:00 219:10:00 220:10:00 221:10:00 222:10:00 223:10:00 224:10:00 225:10:00 226:10:00 227:10:00 228:10:00 229:10:00 230:10:00 231:10:00 232:10:00 233:10:00 234:10:00 235:10:00 236:10:00 237:10:00 238:10:00 239:10:00 240:10:00 241:10:00 242:10:00 243:10:00 244:10:00 245:10:00 246:10:00 247:10:00 248:10:00 249:10:00 250:10:00 251:10:00 252:10:00 253:10:00 254:10:00 255:10:00 256:10:00 257:10:00 258:10:00 259:10:00 260:10:00 261:10:00 262:10:00 263:10:00 264:10:00 265:10:00 266:10:00 267:10:00 268:10:00 269:10:00 270:10:00 271:10:00 272:10:00 273:10:00 274:10:00 275:10:00 276:10:00 277:10:00 278:10:00 279:10:00 280:10:00 281:10:00 282:10:00 283:10:00 284:10:00 285:10:00 286:10:00 287:10:00 288:10:00 289:10:00 290:10:00 291:10:00 292:10:00 293:10:00 294:10:00 295:10:00 296:10:00 297:10:00 298:10:00 299:10:00 300:10:00 301:10:00 302:10:00 303:10:00 304:10:00 305:10:00 306:10:00 307:10:00 308:10:00 309:10:00 310:10:00 311:10:00 312:10:00 313:10:00 314:10:00 315:10:00 316:10:00 317:10:00 318:10:00 319:10:00 320:10:00 321:10:00 322:10:00 323:10:00 324:10:00 325:10:00 326:10:00 327:10:00 328:10:00 329:10:00 330:10:00 331:10:00 332:10:00 333:10:00 334:10:00 335:10:00 336:10:00 337:10:00 338:10:00 339:10:00 340:10:00 341:10:00 342:10:00 343:10:00 344:10:00 345:10:00 346:10:00 347:10:00 348:10:00 349:10:00 350:10:00 351:10:00 352:10:00 353:10:00 354:10:00 355:10:00 356:10:00 357:10:00 358:10:00 359:10:00 360:10:00 361:10:00 362:10:00 363:10:00 364:10:00 365:10:00 366:10:00 367:10:00 368:10:00 369:10:00 370:10:00 371:10:00 372:10:00 373:10:00 374:10:00 375:10:00 376:10:00 377:10:00 378:10:00 379:10:00 380:10:00 381:10:00 382:10:00 383:10:00 384:10:00 385:10:00 386:10:00 387:10:00 388:10:00 389:10:00 390:10:00 391:10:00 392:10:00 393:10:00 394:10:00 395:10:00 396:10:00 397:10:00 398:10:00 399:10:00 400:10:00 401:10:00 402:10:00 403:10:00 404:10:00 405:10:00 406:10:00 407:10:00 408:10:00 409:10:00 410:10:00 411:10:00 412:10:00 413:10:00 414:10:00 415:10:00 416:10:00 417:10:00 418:1

[illegible][illegible]

99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9  
105:VRL10

Database: genbank-new

112:MAM 113:VRI 114:PHG 115:PLN 116:PRI 117:PRI2  
118:ROD 119:SVN 120:JNA 121:VPI

[illegible]

Statistics: Mean 11.101; Variance 4.537; scale 2.44

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	941	81%	181	60	U00528AT	R. japonica mRNA for ole
2	438	69%	133	59	AF0013AA	Arabidopsis thaliana
3	428	41%	166	67	U00506CA	Cytisus medeolensis
4	430	37%	1472	65	SCD1201ES	C. pomonensis mRNA for
5	411	29%	1453	67	U00506ED	Glycine max FAD3-1m
6	333	29%	1449	64	U005032AA	Rapportia americana ole
7	123	10.6	1170	62	U0050119G	Lesquerium thaliana
8	60	6%	1515	61	U005068H	Wheat gamma I for ole
9	39	3.4	1008	65	U005061H	Rice gamma I for ole
10	39	3.4	1008	12	U005061H	Rice gamma I for omega 3
11	28	2.3	1023	67	U00505817	Sesamum indicum omega
12	37	3.2	915	61	U005078H	Synedrella nodiflora
13	32	2.9	1332	68	U005061H	Vigna radiata omega-1
14	33	2.9	1366	68	U005061H	Tobacco leaf mRNA for
15	32	2.8	1306	64	U00507817	Putrefaction of oleum
16	31	3.1	931	67	U005061H	Cyclopentadiene
17	30	2.6	1353	60	U005061H	Blasidia purpurilimbia
18	30	2.6	1353	60	U005061H	Blasidia purpurilimbia
19	30	2.6	1353	60	U005061H	Blasidia purpurilimbia
20	30	2.6	1416	60	U005061H	Blasidia purpurilimbia
21	29	2.5	1336	60	U005061H	Blasidia purpurilimbia
22	29	2.5	1336	60	U005061H	Blasidia purpurilimbia
23	29	2.5	1336	60	U005061H	Blasidia purpurilimbia
24	29	2.5	1336	60	U005061H	Blasidia purpurilimbia
25	29	2.5	1336	60	U005061H	Blasidia purpurilimbia
26	28	2.4	1350	59	U005061H	Arabidopsis thaliana
27	28	2.4	1350	59	U005061H	Arabidopsis thaliana
28	28	2.4	1350	59	U005061H	Arabidopsis thaliana
29	28	2.4	1350	59	U005061H	Arabidopsis thaliana
30	28	2.4	1350	59	U005061H	Arabidopsis thaliana
31	27	2.3	1430	60	U005061H	Arabidopsis thaliana
32	27	2.3	1430	60	U005061H	Arabidopsis thaliana
33	27	2.3	1430	60	U005061H	Arabidopsis thaliana
34	27	2.3	1430	60	U005061H	Arabidopsis thaliana
35	27	2.3	1430	60	U005061H	Arabidopsis thaliana
36	27	2.3	1430	60	U005061H	Arabidopsis thaliana
37	27	2.3	1430	60	U005061H	Arabidopsis thaliana
38	27	2.3	1430	60	U005061H	Arabidopsis thaliana
39	27	2.3	1430	60	U005061H	Arabidopsis thaliana
40	27	2.3	1430	60	U005061H	Arabidopsis thaliana
41	27	2.3	1430	60	U005061H	Arabidopsis thaliana
42	27	2.3	1430	60	U005061H	Arabidopsis thaliana
43	27	2.3	1430	60	U005061H	Arabidopsis thaliana
44	27	2.3	1430	60	U005061H	Arabidopsis thaliana
45	27	2.3	1430	60	U005061H	Arabidopsis thaliana
46	27	2.3	1430	60	U005061H	Arabidopsis thaliana
47	27	2.3	1430	60	U005061H	Arabidopsis thaliana
48	27	2.3	1430	60	U005061H	Arabidopsis thaliana
49	27	2.3	1430	60	U005061H	Arabidopsis thaliana
50	27	2.3	1430	60	U005061H	Arabidopsis thaliana

## ALIGNMENTS

RESULT 1	
LOCUS	PODDECAT 1381 bp DNA
DEFINITION	Podocyte mRNA for alpha-1-desaturase.
	22-MAY-1996







Dec 17 15:03

/home/fuller/dec97/US-08-572-027A-5.rge

5

/home/fuller/dec97/US-08-572-027A-5.rge

[illegible][illegible]















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/home/fuher/dec97/U5-08-572-027A-5.rge

15

Dec 17 15:03

[/home/fuler/dec97/US-08-572-027A-5.rge](http://home/fuler/dec97/US-08-572-027A-5.rge)

4

QHQHPALPHYSESEIMWIRKSMYVDERDYGVNLVEVHNHNTADTHAHLFLATVHYHYHAM

polYA\_site 1440

8 A nucleotides

BASE COUNT	367 a	340 c	371 g	412 t
ORIGIN				

Query Match	28.33	Score 223	IN 64	Length 1440
Best Local Similarity	65.08	Prod. No. 2 06a-299		
Matches	700	Conservative	0	Mismatches 349
			Indels	3
			Delets	2

[illegible][illegible][illegible][illegible]

JOURNAL  
MIDLINE  
REFERENCE

Moist, Plant Microbe Interact. 9 (5), 409-415 (1996)  
3675,2910  
2 (bases 1 to 1170)

AUTHORS	Vera, P.
TITLE	Direct Submission
Submitted (JULIAN 1996)	P. Vera, Universidad Politécnica de Valencia

Valencia, Inst. de Biología Molecular y Genética de Financ. Caméno  
de Vera 14, E-46102 Valencia, SPAIN  
Location/Qualifiers  
1. 1170

```

/organism "lycote-stemon eculeum"
/cultivar "Rutgers"
/tissue type "leaf"
67..1068

```

```

/ gene: "cevl1g"
/ readon_start: 1
/ product: "lipid desaturase-like protein"
/ hit_art: "protein"

```

[illegible]



















/home/fuller/dec97/US-08-572-027A-5.rge















[illegible][illegible]



















Dy	835	TCTTACTGATACAGATTGGTGCGAAGCAAGATTCGTTAAAGGAACATTTGCATAACGCTT	894
Dc	478	GACGAGAGATATATGAGATCATTTGAGCAGAGGTATTCAGTAAGCTCAAGCAGACGACGACGACG	537
Oy	849	CATGAGATCATGAGATCATTTTAAACAAGCTCTTTCCATCAATATTCATCATGACATCTGCC	954
Dc	538	cacca 542	
Oy	954	CATCA 959	
<hr/>			
RESULT 9			
ID	T27012 standard; cDNA; 543 BP.		
AC	T27012;		
DE	10-SEP-1996 (first entry)		
KM	Kappa family acid hydroxylase clone plesq2.		
KM	Kappa family acid hydroxylase; Lesquerelle acid; transgenic plant;		
KM	cloned; seed oil; tobacco; Cloning Resource Journal; October 1994		
KM	sunflower; safflower; cotton; soybean, soybean; peanut; coconut;		
KM	oil palm; corn; ss.		
FN	Lesquerella fendleri.		
FN	Key	Lesquerella fendleri	
FT	misc_difference 83		
ET	/tag_ a		
PT	/note Base n at position 83 is not identified*		
FN	M09410075-AI.		
FD	04-APR-1996.		
PF	25-SEP-1995; 011995.		
FR	26-SEP-1994; US: 314596.		
FR	11-OCT-1994; US: 340982.		
FR	20 SEP 1995; US: 429982.		
PA	(BR007) BROUN P.		
PA	(SOME/) SOMERVILLE C.		
FA	(VLOO/) VAN DE LIND F J.		
F1	Brown P., Somerville C., Van De Lind F.J.		
DR	MF1, 96-200914/20.		
PT	Prod'n. of hydroxylated fatty acids, e.g. linolenic or linopentonic		
PT	acid - in genetically modified plants such as rapeseed, flax,		
PT	sunflower or cotton, cont'a fatty acid hydroxylase gene.		
PS	Claim 4; Page 65 66; 10pp; English.		
CC	CDNA clones plesq2 (T27012) and plesq3 (T27013) were obsd. from a		
CC	Lesquerella fendleri library by PCR amplification using primers		
CC	(see also T27011). Found no regions of homology between cDNA T2701		
CC	hydroxylase and the Arabidopsis delta desaturase (Fat1). The gene		
CC	corresponding to plesq2 is highly and specifically expressed in		
CC	seeds of L. fendleri. A genomic clone, plesq Hyd (T27011), was		
CC	isolated using plesq2 as probe, and shown to encode a kappa family		
CC	acid hydroxylase (K27013). Transgenic plants that express plesq2		
CC	contain altered levels of hydroxylated fatty acids, e.g. lesquerell		
CC	acid (14 hydroxy 17 hexanoic acid), in seed oils, waxes and		
CC	related products.		
SQ	Sequence: 543 BP, 100 %; 100 %; 100 %; 100 %; 100 %;		
<hr/>			
Query Match:	22.9%, Score 279, EG 27, length 532,		
Rest Local Similarity:	76.8%, Pos'd Pos: 144/189;		
Matches 414, Conservative 9, Mismatches 122, Indels 3, Gaps 17,			
<hr/>			
Dc	7	CACGAGAGATATATGAGATCATTTGAGCAGAGGTATTCAGTAAGCTCAAGCAGACGACGACGACG	537
Oy	421	CATGAGATCATGAGATCATTTTAAACAAGCTCTTTCCATCAATATTCATCATGACATCTGCC	480
Dy	481	AACAGATCATGAGATCATTTTAAACAAGCTCTTTCCATCAATATTCATCATGACATCTGCC	546

D8	127	ggttaagatggtagtgcctcctcccggttcgacttggaacaaagcatgatgacgagt	186
Q9	541	ATGTAAACAGTAAAGTAATAATGTTGGCTGAATCTTAACTTAAAGTCGTCCCA	600
D8	187	ggagcatatgagggt--tttgtaccattcttcccaatcagagcagacctaacgagac	243
Q9	601	AAGATTAAACAAGCGAAGCCTTGCTGCGCATTTGCACCAATGCTTAAATTAAC	660
D8	244	ccttgagagctcccgagatacagctcccgaggtggtgctagctgctgttatggtct	303
Q9	441	CGGAGGAGGCTCAAGAATAATCGAACAGCTGAATGAGCTGCTGCTGCTGCTGCT	720
D8	304	tacggctttagctggtctaaaaggcttgactgctatgctgctgctcagggagtagcct	363
Q9	721	TTCGGCTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	789
D8	364	tggagagtgatctctctctctctctctctctctctctctctctctctctctctct	423
Q9	781	CATATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	840
D8	428	ccccctctctctctctctctctctctctctctctctctctctctctctctctctct	483
Q9	841	CCTACTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
D8	484	gagctgagctctctctctctctctctctctctctctctctctctctctctctctctct	542
Q9	901	GAAATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	959
RESULT	10		
ID	066072	standard; cDNA; 673 BP.	
AC	066072		
DT	09-NOV-1994	(first entry)	
DE	Description of entry: messenger RNA from stage 12 heart tissue. In the cDNA of plasmid pRF2-1C.		
KM	Fatty acid desaturase lipid, unsaturated, transgenic plant; ss.		
CS	Ruminants communs.		
FN	very	Transcript quality score	
FT	CDS	1..673	
FT	/+flag_a		
FN	M09411516-A.		
PR	26 MAY-1994.		
PR	15-OCT-1993; 0009487.		
PR	15-OCT-1993; 0009334		
PA	(map) DU POINT DE NEMOURS & CO E.L.		
PI	Liggett AP, Okley JG;		
PR	WFL 34:182515/22.		
PR	P 69DB; R54011.		
DE	Characterization of fatty acid synthase cDNA from sheep - Fatty acid synthesis of plant lipid deposition		
E3	Chen Y, Rep 199, 1479, English.		
CC	Polysomal mRNA was isolated from castor beans at stages 1-11 (7 to 12 DAP) and analyzed by RT-PCR (stage 1: stage 10-12 DAP).		
CC	In all of each mRNA was used for separate PCR reactions.		
CC	The reverse transcriptase reaction was primed with random hexamers and the PCR reaction with degenerate delta-12 desaturase primers NF2 and NF9 (NF60NTS, Q660T6). A DNA fragment of approx. 300 bp was amplified from both stage 1-11 and stage 10-12 DAP.		
CC	IV mRNA. The amplified DNA fragment from one of the reactions was gel purified and cloned into a vector to create plasmid FRP1. The 100 bp insert in FRP2 was sequenced (Q660T2).		
CC	An isolated nucleic acid fragment wherein the nucleic acid identity is not required to sequence Q660T1 is claimed. A method to		







[illegible]

RESULT	12
ID	Q10572 standard; RNA; 1047 BP.
AC	Q10572;
DT	09-APR-1991 (first entry)
DE	Human Natriuretic Peptide Receptor B.
KW	NPRB; ANP; BRN; CNRP; kidney failure; heart failure; protein kinase
KM	hyperaldosteronism; glaucoma; guanyl cyclase.
OS	Homo sapiens.
EH	Key Location/Qualifiers
FT	Peptide 1..22
FT	/label= signal sequence
FT	Protein 12
FT	/label= mature NPRB
FT	Domain 73..455
FT	/label= extracellular domain
FT	/note= "binds natriuretic peptide A, B and C"
FT	Domain 456..456
FT	/label= transmembrane domain
FT	Domain 479..1047
FT	/label= cytoplasmic domain
FT	/note= "GC and protein kinase activity"
FT	Modified-site 24..26
FT	/label= N-glycos site
FT	Modified-site 35..37
FT	/label= N-glycos site
FT	Modified-site 161..163
FT	/label= N-glycos site
FT	Modified-site 195..197
FT	/label= N-glycos site
FT	Modified-site 244..246
FT	/label= N-glycos site
FT	Modified-site 277..279
FT	/label= N-glycos site
FT	Modified-site 349..351
FT	/label= N-glycos site
FT	Modified-site 400..402
FT	/label= N-glycos site
FM	Wojcik792.A.
PD	10-JAN-1991.
PR	ZF-MN-1989; UNK06.
PR	23-JUN-1989; US-370673.
FA	(GSTR) GENPEPTIDE INC.
P1	Chang M, Goodell D, Lowe D;
DR	WPI; 91-03671/05.
DR	N-PSSDB; Q10324.
ST	Natriuretic peptide receptor B - for diagnosis and treatment of
PT	kidney failure, heart failure, hyperaldosteronism, glaucoma etc.
PS	Claim 3; Fig 1; 4pp; English
CC	The sequence was derived from the DNA encoding natriuretic peptide
CC	receptor B, NPRB, having guanyl cyclase (GC) activity and protein
CC	kinase activity. The DNA can be inserted into expression vectors
CC	for the production of the protein, after being inserted to produce
CC	NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=
CC	114,972). The protein (or variants) can be used in treatment of
CC	natriuretic peptide disorders, and also to isolate peptides using
CC	affinity chromatography. Antibodies with affinity for NPRB can
CC	also be prepd.
SQ	Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;
Query Match	5.6%; Score 65; DB 2; Length 1047;
Best local similarity	9.4%; Ref. No. 9,296,27;
Motifs	59; Conserved 29; W607-3406 449; motifs 7; Cps 7;



[illegible][illegible]



Best Local Similarity 15.0%; Pied. No. 2,456 12;  
Matches 18; Conservative 59; Mismatches 46; Indels 1; Gaps 1;

[illegible]

## RESULT 15

ID Q51746 standard; cDNA; 91 R<sup>1</sup>.

NC Q51746;

31 MAY-1994 (first entry)

DE. Oligonucleotide probe MK14 A

oligonucleotide DNA probes; mycobacterial disease diagnosis;

SS	SS
SS	SS

US Synthetic.  
IN EO 671011

IN 511911-A.  
ON 01 DEC 1993

FD-01-DEC-1993  
01 MAY-1993

26 MAY 1997; 115-8896

PR 46-MAY-1992; US--889651

MA (BROU) HEDIN DICKINSON CO.  
21 Shook Dr. Seattle WA:

WP1 - 93-37884A/48

DR M21; 93-516644/46  
 IT Now olitru:ent)out

37 detection and amplification of *Mycobacteria* nucleic acid in

PT samples

PS Claim 3: Page 14: 23pp: English

of 0.1 g/cm<sup>3</sup> and 1.4 g/cm<sup>3</sup> (M<sub>1</sub> and M<sub>2</sub>)

(051735). It hybridized to all spp. of mycobacteria tested, but

cross reacted to a few non-mycobacterial spp. The probe may have

be useful as an initial screen for mycobacterial infection.

See also Q51735-45 and Q51747-59.

50 Sequence 91 BP: 5 A: 17 C: 15 G: 4 T:

Query Match	Score	PR	Q	Length
1	66	9	91	

Best Local Similarity 11.7%; Error No 1.03e 11;

Matches	7	Conservative	44	Mismatches	9	Indels	0	Gaps	0
---------	---	--------------	----	------------	---	--------	---	------	---

Db 4 tccgcgscvrrsyvvrrrrrbh.....bhrrrbhbhgsvrrrbhbvrbbvbhvbhrrrvsvctc 63

Country	Year	Value	Unit
Algeria	2000	1.00	1000
Algeria	2001	1.00	1000
Algeria	2002	1.00	1000
Algeria	2003	1.00	1000
Algeria	2004	1.00	1000
Algeria	2005	1.00	1000
Algeria	2006	1.00	1000
Algeria	2007	1.00	1000
Algeria	2008	1.00	1000
Algeria	2009	1.00	1000
Algeria	2010	1.00	1000
Algeria	2011	1.00	1000
Algeria	2012	1.00	1000
Algeria	2013	1.00	1000
Algeria	2014	1.00	1000
Algeria	2015	1.00	1000
Algeria	2016	1.00	1000
Algeria	2017	1.00	1000
Algeria	2018	1.00	1000
Algeria	2019	1.00	1000
Algeria	2020	1.00	1000
Algeria	2021	1.00	1000
Algeria	2022	1.00	1000
Algeria	2023	1.00	1000
Algeria	2024	1.00	1000
Algeria	2025	1.00	1000
Algeria	2026	1.00	1000
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Algeria	2028	1.00	1000
Algeria	2029	1.00	1000
Algeria	2030	1.00	1000
Algeria	2031	1.00	1000
Algeria	2032	1.00	1000
Algeria	2033	1.00	1000
Algeria	2034	1.00	1000
Algeria	2035	1.00	1000
Algeria	2036	1.00	1000
Algeria	2037	1.00	1000
Algeria	2038	1.00	1000
Algeria	2039	1.00	1000
Algeria	2040	1.00	1000
Algeria	2041	1.00	1000
Algeria	2042	1.00	1000
Algeria	2043	1.00	1000
Algeria	2044	1.00	1000
Algeria	2045	1.00	1000
Algeria	2046	1.00	1000
Algeria	2047	1.00	1000
Algeria	2048	1.00	1000
Algeria	2049	1.00	1000
Algeria	2050	1.00	1000
Algeria	2051	1.00	1000
Algeria	2052	1.00	1000
Algeria	2053	1.00	1000
Algeria	2054	1.00	1000
Algeria	2055	1.00	1000
Algeria	2056	1.00	1000
Algeria	2057	1.00	1000
Algeria	2058	1.00	1000
Algeria	2059	1.00	1000
Algeria	2060	1.00	1000
Algeria	2061	1.00	1000
Algeria	2062	1.00	1000
Algeria	2063	1.00	1000
Algeria	2064	1.00	1000
Algeria	2065	1.00	1000
Algeria	2066	1.00	1000
Algeria	2067	1.00	1000
Algeria	2068	1.00	1000
Algeria	2069	1.00	1000
Algeria	2070	1.00	1000
Algeria	2071	1.00	1000
Algeria	2072	1.00	1000
Algeria	2073	1.00	1000
Algeria	2074	1.00	1000
Algeria	2075	1.00	1000
Algeria	2076	1.00	1000
Algeria	2077	1.00	1000
Algeria	2078	1.00	1000
Algeria	2079	1.00	1000
Algeria	2080	1.00	1000
Algeria	2081	1.00	1000
Algeria	2082	1.00	1000
Algeria	2083	1.00	1000
Algeria	2084	1.00	1000
Algeria	2085	1.00	1000
Algeria	2086	1.00	1000
Algeria	2087	1.00	1000

CP 1106 TCGCTTCAATATGATATTTATTTCTCTCAATAGCTTAAAGAGGCTTTT 1047

Search completed: Wed Dec 17 14:25:13 1998  
Job time : 227 secs.



(f)



































CC	isolate/nucleic acid fragments encoding fatty acid desaturases	CC	isolate/nucleic acid fragments encoding fatty acid desaturases
CC	and related enzymes is claimed which comprises: comparing AA	CC	sequences in R03697-R03702 and other fatty acid desaturase sequences;
CC	sequences in R03697-R03702 and other fatty acid desaturase sequences;	CC	identifying conserved sequences of 4 or more bases distal and adjacent to
CC	oligos based on the conserved sequences; and using the oligos to	CC	isolate sequences encoding fatty acid desaturases and
CC	desaturase-related enzymes.	CC	desaturase-related enzymes.
CC	Sequence 673 BP; 154 A; 169 C; 150 G; 200 T;	CC	Sequence 673 BP; 154 A; 169 C; 150 G; 200 T;
CC	Query Match	CC	Query Match
CC	Best Local Similarity 70.3%; Pos. No. 1,330-1667	CC	Best Local Similarity 70.3%; Pos. No. 1,330-1667
CC	Matches 471; Conservative 0; Mismatches 146; Indels 3; Gaps 2;	CC	Matches 471; Conservative 0; Mismatches 146; Indels 3; Gaps 2;
Dh	1 tgggtgatggcagatgattggggagaaagtcctcagtgatcaatgattgatgat 60	Dh	1 tgggtgatggcagatgattggggagaaagtcctcagtgatcaatgattgatgat 60
Gy	301 tgggtgatgagatgagatggggagaaagtcctcagtgatcaatgattgatgat 360	Gy	301 tgggtgatgagatgagatggggagaaagtcctcagtgatcaatgattgatgat 360
Dh	61 gtagtgatgattatgctaaactgctgctgtgcttcttcttcttcttcttctt 120	Dh	61 gtagtgatgattatgctaaactgctgctgtgcttcttcttcttcttcttctt 120
Gy	161 gtagtgatgattatgctaaactgctgctgtgcttcttcttcttcttcttctt 420	Gy	161 gtagtgatgattatgctaaactgctgctgtgcttcttcttcttcttcttctt 420
Dh	121 cctgcgcgcatcatcatcaaacagagttcctggagacgagtgatgcttccagag 180	Dh	121 cctgcgcgcatcatcatcaaacagagttcctggagacgagtgatgcttccagag 180
Gy	421 cctgcgcgcatcatcatcaaacagagttcctggagacgagtgatgcttccagag 480	Gy	421 cctgcgcgcatcatcatcaaacagagttcctggagacgagtgatgcttccagag 480
Dh	181 aaggaatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 240	Dh	181 aaggaatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 240
Gy	481 aaggaatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 540	Gy	481 aaggaatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 540
Dh	241 aacatcggcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 300	Dh	241 aacatcggcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 300
Gy	541 aacatcggcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 600	Gy	541 aacatcggcgctgctgctgctgctgctgctgctgctgctgctgctgctgct 600
Dh	301 agggatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 360	Dh	301 agggatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 360
Gy	601 agggatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 660	Gy	601 agggatcagatcagctgctgctgctgctgctgctgctgctgctgctgctg 660
Dh	358 cgcgagcgatcagatcagatcagatcagatcagatcagatcagatcagat 417	Dh	358 cgcgagcgatcagatcagatcagatcagatcagatcagatcagatcagat 417
Gy	640 cgcgagcgatcagatcagatcagatcagatcagatcagatcagatcagat 700	Gy	640 cgcgagcgatcagatcagatcagatcagatcagatcagatcagatcagat 700
Dh	418 taacaaactgctatcagcagaggtgctgttggttcgctgctgctgctgctg 477	Dh	418 taacaaactgctatcagcagaggtgctgttggttcgctgctgctgctgctg 477
Gy	721 ttaacaaactgctatcagcagaggtgctgttggttcgctgctgctgctgctg 780	Gy	721 ttaacaaactgctatcagcagaggtgctgttggttcgctgctgctgctgctg 780
Dh	478 ttggtggtgattatcctgctgctgctgctgctgctgctgctgctgctgctg 537	Dh	478 ttggtggtgattatcctgctgctgctgctgctgctgctgctgctgctgctg 537
Gy	781 ttggtggtgattatcctgctgctgctgctgctgctgctgctgctgctgctg 840	Gy	781 ttggtggtgattatcctgctgctgctgctgctgctgctgctgctgctgctg 840
Dh	538 cccatcatgattcctgagcagggggtggtggtggtggtggtggtggtggtg 597	Dh	538 cccatcatgattcctgagcagggggtggtggtggtggtggtggtggtggtg 597
Gy	841 cccatcatgattcctgagcagggggtggtggtggtggtggtggtggtggtg 900	Gy	841 cccatcatgattcctgagcagggggtggtggtggtggtggtggtggtggtg 900
Dh	598 gattcagggatcctgagcaggggtggtggtggtggtggtggtggtggtggt 657	Dh	598 gattcagggatcctgagcaggggtggtggtggtggtggtggtggtggtggt 657
Gy	901 gattcagggatcctgagcaggggtggtggtggtggtggtggtggtggtggt 960	Gy	901 gattcagggatcctgagcaggggtggtggtggtggtggtggtggtggtggt 960
Dh	658 atttctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 717	Dh	658 atttctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 717
Gy	961 atttctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 1020	Gy	961 atttctctcttcttcttcttcttcttcttcttcttcttcttcttcttct 1020

Dec 17 15:30

/home/fueller/dec97/US-08-572-027A-3.mg

20

[illegible]



[illegible][illegible]







FT misc:leisure 19...69  
FT /\*tag= a  
FT /function= multiple cloning site  
FT primer bind 187..204  
FT /\*tag= b  
PD EP-785123-A  
PD 05-MAY-1988  
PF 30-MAR-1988; 105163.  
PR 03-APR-1987; uc-034819.  
PA (SUSO) STOMEN SOKERI OY.  
P1 Lehtovaara P, Knowles J, Koivola A, Bamford J, Reinikainen T;  
P2 WP17\_88-279927/40.  
L1 Introducing random point mutations into nucleic acids  
P1 by means of single stranded template, annealing a primer, elongation,  
P2 misincorporation, completion of molecules and screening  
P3 disclosure; p; English.  
CC Random point mutations were introduced into the alpha fragment of  
CC *E. coli* beta-galactosidase. The wild type sequence was obtained as a  
CC single stranded template and an oligonucleotide was hybridised to  
CC it to generate a form of DNA molecules which terminate at all  
CC possible nucleotide positions within a specified region. The  
CC variable 3' ends generated in this way are used as primers for  
CC reverse transcriptase. Nucleotides are misincorporated by the  
CC transcriptase and the molecules are completed to forms that can be  
CC amplified and then expressed in a suitable host vector system.  
CC The sequence covers all 176 different substitutions, most of which  
CC occurred singularly in any given mutant.  
CC See also p00575.  
CC Sequence 204 BP; 21 Ap 47 G; 17 G; 11 T; 108 others;

Query Match	3.6%;	Score 41;	DB 1;	length 204;
Best Local Similarity	14.2%;	Pred. No. 4.69e-11;		
Matches	17;	Conservative	59;	Mismatches 43;
				Indels 1;
				Gaps 1

[illegible]

Search completed. Wed Dec 17 15:30:50 1997  
Job time : 233 secs.































[illegible]















```

EN    EF-7191-A;
PB    01 DEC-1993.
PE    24-MAY-1993; 108325.
PK     Z6-MAY-1992; US-889651.
PA    (BECT ) SECTON DICKINSON CO.
PI    Shank DD, Spears PA;
PR    WFLI 93-37884/48.
PT     New oligonucleotide probes specific for Mycobacteria - used for
ET      detection and amplification of Mycobacteria nucleic acid in
FT       samples
PS    Claim 3; Page 14; 23pp; English.
CC    Oligonucleotide probe MK14A consists of nucleotides 5'-9' of MK14
CC    Q(51735). It hybridized to all spp. of mycobacteria tested, but
CC    cross reacted to a few non-mycobacterial spp. The probe may
CC    be useful as an initial screen for mycobacterial infection.
CZ    See also Q(51735-45) and Q(1747-59).
SQ     Sequence   91 BP;   5 A;   17 C;   15 G;   4 T;
Lc         Query Match          3.6%; Score 42; DB 9; Length 91;
Sest Local Similarity 11.7%; Pwd No. 1 R3s-11;
Matches    7; Conservative 44; Mismatches 9; Indels 0; Gaps 0;
lc         4 tccgcgssvhyvvshhvshbvvhvsvvvvhvhhvshbhvyhsyvc 63
||||| : :::: : ..... : .....,..... ||
II06 proctiaaaafaatatatttttcttcctttaataaacgttttaacacctggagtga 104
```

Search completed: Wed Dec 17 17:25:06 1998  
Job time : 153 secs.

Search completed: Wed Dec 17 17:25:06 1998  
Job time : 153 secs.











PS Claim 3 Page 116-118; 147pp; English.

CC The gene sequence of Gm-4 was identified by screening with frag

CC cDNA library made with poly A mRNA from developing B. napus seeds

CC with radiolabeled pPCR with nucleotide fragments derived from

CC plasmid 1650, designated pPCR-1650, was sequenced (0660649). Plasmid

CC pPCR-1650 was designed as overhang 15, 1647 with the ATCC and more

CC accession number ATCC 69294. An isolated nucleic acid fragment

CC wherein the nucleic acid identity is 90% or greater to

CC 0660649 is claimed.

CC Sequence 1234 BP; 320 A; 300 C; 455 G

Query Match 93.98; Score 1004; FR 10; Length 1344;

Best Local Similarity 97.6%; Pval No. 0.00e+00;

Matches 112; Conservative 9; Variations 25; Indels 2; Gaps 2

[illegible][illegible]

RESULT	2
AC	Accession J, NCBI 2473 BP.
AC	066074
DT	04-NOV-1994 (first entry)
DE	Sequence of microsomal delta-12 desaturase gene.
FW	Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.
OS	Arabidopsis thaliana.
Key	Location/Qualifiers
FT	exon
FT	/ft 99= a
FT	intron
FT	/ft 99= b
PN	MD941516 A.
PS	26-MAY-1994.
FE	15-OCT-1993; 0004981.
FR	17 NOV 1992; 95-911349.
PA	(DDBO ) DU PONT DE NEMOURS & CO E. I.
P1	highway at Okaley JJ;
PR	WPI 94-183515/22.
PT	Genes for fatty acid desaturase enzymes - permit alteration of
PT	plant lipid composition
PS	claim by Page 156-138; 147pp English.
CC	The gene coding for delta12 was isolated by screening Arabidopsis
CC	genomic DNA library using radiolabeled cDNA insert, purifying
CC	positively hybridising plaque, and subcloning a 6kb Hind III insert
CC	fragment from the phage DNA in pBlue-script vector. Comparison of the
CC	sequence of the gene (066074) and the cDNA (066088) revealed the
CC	presence of a single intron of 1134 bp at a position between
CC	8 nucleotides 88 and 89 of the cDNA, which is 4 nucleotides 9' to the
CC	initiation codon. The cDNA is contained in clone p2103. Plasmid
CC	p2103 was deposited on October 16, 1992 with the ATCC and bears
CC	accession number AF06 60094. An isolated nucleic acid treatment







[illegible][illegible]











[illegible][illegible]



























































[illegible][illegible]



Dec 17 11:05

/home/fuler/dec97/US-08-572-027A-4.ppt

[illegible]

ENTRY	RESULT
JC2555	#type complete
One is 3' entry and 3' entry	2000-10-10 (10-10)
#formal name: Nicotiana glauca	#common name: common tobacco
14-May-1995	14-May-1995

Accessions	Reference
JC2555	Hamada, T., Kodama, H., Nishimura, M., Ito, K.
JC2555	Gene (1994) 147:293-294
Journal	Cloning of a cDNA encoding tobacco omega-3 fatty acid
Title	desaturase.

```
##status      preliminary
##residues    1-379 ##label HAM
##cross-references DDBJ:J025509
          ##length 379 ##method
```

**SUMMARY** #length 379 #mc.locations 44249 #mc.locations 1240

Query Match	22.6%;	Score: 79;	Length: 339;
Best Local Similarity	38.2%;	Pred. No. 1, two-106;	
Matches	12%;	Mismatches: 96;	Indels: 20;
			Gaps: 14;

[illegible][illegible]

Dd 245 l f m e d i d e n t y / h b h g k k l w r g s c w e y n g l t e u d o j f m a l h a d - g y t u h 390  
 : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
 Qy 263 l v n z c a l l t r a d t r c a n t e n t e m e a l a n e d o j f m a l h a d - g y t u h 390  
 : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
 Dd 304 h l f p q p y n l e a t k a p t g y n 330  
 : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
 Qy 320 H R E S T M E A M E T A L I C E Y N 345  
 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT	ENTRY	TITLE	ORGANISM
5	S52650	destrinase delta 1b	<i>Synchytrium</i> sp. (strain F776683)
		#formal name	<i>Synchytrium</i> sp.

DATE	26-Oct-1986	##sequence_revision	28 Oct 1986	##ext_change
ACCESSIONS	S52600			
REFERENCE	S52649			
AUTHORS	Okamoto, M.; Ito, D.A.; Higuchi, O.; Wada, H.; Nishida, I.; Shimizu, M.; Ito, T. (1986) FEBS LETT 197:1-5			
##protein	Cloning of omega-3 desaturase from <i>Gyrodactylus</i> and its use in altering the degree of membrane unsaturation.			
##title				
##accession	S52650			
##status	preliminary			
##ridos	1-359	##label	SNK	
##cross-references	CR:P13780			
SUMMARY	length 359	##molecular-weight	41919	##checksum 9162

[illegible]

26 74 wagtifistivohzhojgistskinnwghstplpygwshrbhang 1  
1 | | : : |::||| || :: : : : ||| : : |||::|||  
90 WAGTIFISTIVOHZHOJGISTSINNWGHSTPLPYGWSHRBHANG 14

[illegible][illegible][illegible]

RESULT	6
ENTRY	102319
TITLE	alpha-2 fatty acid desaturase (EC 1.14.99) - GMD - soybean
SEQUENCE	100 amino acids, 10716 daltons, 100% soybean
DATE	28 Oct 1993
	SwissProt accession: P03474, Prot-Change
	21-Mar-1996

**REFERENCE**

# Authors

102335  
Yedda, N.S., Mierzbicki, A.J., Angelini, M., Gastor, C.S.  
Fennell, T.L., Erickson, A.T., Brown, W.E., Roth, J.L.,  
Schweigerl, R., Stecco, K.L., Allen, S.M., Blackwell, H.  
Pattner, B.S., Carlson, F.F., Passelli, S.H., Pattamann,  
Eleanor, E.J., Browne, J.  
Plant Physiol. (1994) 103:467-476

\* Journal

Accession	Gene	Label	Yeast
JQ2339	1-453	1-453	YAL001
JQ2340	1-453	1-453	YAL002
JQ2341	1-453	1-453	YAL003
JQ2342	1-453	1-453	YAL004
JQ2343	1-453	1-453	YAL005
JQ2344	1-453	1-453	YAL006
JQ2345	1-453	1-453	YAL007
JQ2346	1-453	1-453	YAL008
JQ2347	1-453	1-453	YAL009
JQ2348	1-453	1-453	YAL010
JQ2349	1-453	1-453	YAL011
JQ2350	1-453	1-453	YAL012
JQ2351	1-453	1-453	YAL013
JQ2352	1-453	1-453	YAL014
JQ2353	1-453	1-453	YAL015
JQ2354	1-453	1-453	YAL016
JQ2355	1-453	1-453	YAL017
JQ2356	1-453	1-453	YAL018
JQ2357	1-453	1-453	YAL019
JQ2358	1-453	1-453	YAL020
JQ2359	1-453	1-453	YAL021
JQ2360	1-453	1-453	YAL022
JQ2361	1-453	1-453	YAL023
JQ2362	1-453	1-453	YAL024
JQ2363	1-453	1-453	YAL025
JQ2364	1-453	1-453	YAL026
JQ2365	1-453	1-453	YAL027
JQ2366	1-453	1-453	YAL028
JQ2367	1-453	1-453	YAL029
JQ2368	1-453	1-453	YAL030
JQ2369	1-453	1-453	YAL031
JQ2370	1-453	1-453	YAL032
JQ2371	1-453	1-453	YAL033
JQ2372	1-453	1-453	YAL034
JQ2373	1-453	1-453	YAL035
JQ2374	1-453	1-453	YAL036
JQ2375	1-453	1-453	YAL037
JQ2376	1-453	1-453	YAL038
JQ2377	1-453	1-453	YAL039
JQ2378	1-453	1-453	YAL040
JQ2379	1-453	1-453	YAL041
JQ2380	1-453	1-453	YAL042
JQ2381	1-453	1-453	YAL043
JQ2382	1-453	1-453	YAL044
JQ2383	1-453	1-453	YAL045
JQ2384	1-453	1-453	YAL046
JQ2385	1-453	1-453	YAL047
JQ2386	1-453	1-453	YAL048
JQ2387	1-453	1-453	YAL049
JQ2388	1-453	1-453	YAL050
JQ2389	1-453	1-453	YAL051
JQ2390	1-453	1-453	YAL052
JQ2391	1-453	1-453	YAL053
JQ2392	1-453	1-453	YAL054
JQ2393	1-453	1-453	YAL055
JQ2394	1-453	1-453	YAL056
JQ2395	1-453	1-453	YAL057
JQ2396	1-453	1-453	YAL058
JQ2397	1-453	1-453	YAL059
JQ2398	1-453	1-453	YAL060
JQ2399	1-453	1-453	YAL061
JQ2400	1-453	1-453	YAL062
JQ2401	1-453	1-453	YAL063
JQ2402	1-453	1-453	YAL064
JQ2403	1-453	1-453	YAL065
JQ2404	1-453	1-453	YAL066
JQ2405	1-453	1-453	YAL067
JQ2406	1-453	1-453	YAL068
JQ2407	1-453	1-453	YAL069
JQ2408	1-453	1-453	YAL070
JQ2409	1-453	1-453	YAL071
JQ2410	1-453	1-453	YAL072
JQ2411	1-453	1-453	YAL073
JQ2412	1-453	1-453	YAL074
JQ2413	1-453	1-453	YAL075
JQ2414	1-453	1-453	YAL076
JQ2415	1-453	1-453	YAL077
JQ2416	1-453	1-453	YAL078
JQ2417	1-453	1-453	YAL079
JQ2418			



















(a) (b) (c) (d) (e) (f)

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```

Misch_pp         received.  python database search, using Smith-Waterman algorithm
Run on:          Mel Dec 13 11:13:44 1997.  Master file: 13 04 1997
                795,703 Million cell updates/sec
Tabular output not generated.

```

```
Title:      05-02-070-0072-6
Description: (1-084) From 05-05720278-6.pcp
Perfect Score: 30.27
Sequence:   1 MAAHMAHMAHSEPPSSASHLN.....TVETPTGTRKNVWNNHKL 304
```

Sealed:	9106 bags, 235632.2 pounds
Scoring table:	FAM 150
	Gap 11

Post-processing: Minimum Match 0%  
Listing first 45 summaries

1:ann1 2:ann2 3:ann3 4:ann4 5:annan1 6:annan2 7:annan3  
8:annan4 9:annan5 10:annan6 11:annan7 12:annan8  
13:annan9 14:annan10 15:unenc 16:unrev

Christina: Mom, 46.871; William 172.960; Sean 11.454

pred.  $H_0$  is the number of results predicted by chance for a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

## SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	798	26.4	317	5	smg3-3 fatty acid	2,976-17
2	793	26.2	345	5	smg3-3 fatty acid	2,976-11
3	776	25.6	333	5	smg3-3 fatty acid	3,736-11
4	733	24.2	319	15	smg3-3 fatty acid	3,660-10
5	711	23.3	423	5	smg3-3 fatty acid	4,440-10
6	706	23.3	404	5	smg3-3 fatty acid	3,750-10
7	701	23.2	390	5	smg3-3 fatty acid	3,160-10
8	703	23.2	445	5	smg3-3 fatty acid	1,750-10
9	696	23.0	353	15	desaturase	2,450-10
10	473	9.0	341	15	smg3-3 fatty acid	4,750-14
11	267	6.6	311	15	smg3-3 fatty acid	4,750-14
12	251	6.3	447	16	smg3-3 fatty acid	2,786-22

13	244	8.1	351	554559	Dolich-12 deacetylase (	3.91e-21
14	239	7.9	447.10	549333	n-6 fatty acid desat	2.44e-20
15	223	7.7	339.14	547950	1- $\alpha$ ,25-dihydroxyvitamin	2.05e-19
16	216	7.1	381.9	511119	steroid C6a desatur	1.13e-14
17	132	4.4	358	554559	1- $\alpha$ ,25-dihydroxyvitamin	2.42e-09
18	113	3.7	359.16	535157	hepatic 1 $\alpha$ -OH dehydro	6.35e-02
19	104	3.4	400.11	150130	isochlorogenic receptor -	4.70e-04
20	132	3.4	535.11	555441	probiotic component pr	1.76e+00
21	103	3.4	537.10	564432	hypothetical protein	4.70e+00
22	99	3.3	93.10	564463	hypothetical protein	2.75e+00
23	100	3.3	224	149149	socii protein - Chlam	2.13e+00
24	109	3.3	216	544953	ammonia monooxygenas	2.13e+00
25	100	3.3	457.16	514488	sexP protein - Chlam	2.13e+00
26	103	3.3	702.8	503932	hypothetical protein	1.64e+00
27	94	3.2	140.14	524043	oxyanion receptor -	3.54e+00
28	98	3.2	186.14	524043	oxyanion receptor -	3.54e+00
29	98	3.2	389.14	554497	oxyanion receptor -	3.54e+00
30	98	3.2	389.14	554497	oxyanion receptor -	3.54e+00
31	98	3.2	419.14	104742	oxyanion receptor -	3.54e+00
32	98	3.2	424.13	561984	hypothetical protein	3.54e+00
33	96	3.2	485.14	561987	nitrogen receptor	3.54e+00
34	98	3.2	522.1	559797	RNA directed RNA pol	3.56e+00
35	96	3.2	2336.14	544386	omega-oxo-acyl-CoA sh	5.91e+00
36	97	3.1	77.10	539636	hypothetical protein	2.58e+00
37	95	3.1	222.14	140495	cytochrome b5 reductase	1.58e+00
38	93	3.1	418.15	513731	hypothetical protein	4.70e+00
39	92	3.0	115.10	564354	hypothetical protein	1.59e+00
40	91	3.0	795.9	564134	disproportionate	2.02e+00
41	91	3.0	439.4	513985	sexP protein - Chlam	2.02e+00
42	92	3.0	477.10	564100	oxyanion receptor	1.59e+00
43	91	3.0	498.12	503197	4-aminobutyrate 1,4-	2.02e+00
44	92	3.0	539.12	558497	oxyanion receptor -	1.59e+00
45	92	3.0	466.11	558493	PF709 protein - ynf	1.59e+00

## ALIGNMENTS

```
ENTRY      1
TITLE      omega-3 fatty acid desaturase (EC 1.14.99.-) RN3 - tape
ORGANISM   #journal name Brassica napus #common name rape
DATE       31-Mar-1998 #revision #revision 20 Nov 1994 #last change
          21-Mar-1996
APPEAREDS  #pubmed
REFERENCE  #pubmed
          702337
          702335
          702333
Yildiz, N.S.; Mutsaers, A.; Agreffer, M.; Guterl, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schwinger, R.; Stewer, K.F.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldman, K.A.;
Pierce, J.; Browse, J.
Plant Physiol. (1993) 103:467-476
Cloning of higher plant omega-3 fatty acid desaturases.
#journal    #journal 10
#contents   702337
#keywords    #RNA;BNS
#postscript 1-377 ##label YAD
#misc       1-156 reference 20:229462
COMMENT     This enzyme introduces the third double bond in the biosynthesis of
16:3 and 18:3 fatty acids which are important constituents of
plant membranes.
#accession  #accession 702337 #fatty acid desaturase
#definition #definition 1-carbon weight class #molecular weight
```



Query Match	Score	Pos	Length
Best Local Similarity	39.4%	Pos: 102-292	190
Matches	135	Conservative	74
		Mismatches	105
		Indels	24
		Gaps	18

Db	Accession	Score	Pos	Length
2	U00001	39.4%	102-292	190
9	U00002	39.4%	102-292	190
62	U00003	39.4%	102-292	190
58	U00004	39.4%	102-292	190
115	U00005	39.4%	102-292	190
128	U00006	39.4%	102-292	190
170	U00007	39.4%	102-292	190
188	U00008	39.4%	102-292	190
224	U00009	39.4%	102-292	190
246	U00010	39.4%	102-292	190
264	U00011	39.4%	102-292	190
304	U00012	39.4%	102-292	190

Result	Accession	Score	Pos	Length
2	U00001	39.4%	102-292	190
9	U00002	39.4%	102-292	190
62	U00003	39.4%	102-292	190
58	U00004	39.4%	102-292	190
115	U00005	39.4%	102-292	190
128	U00006	39.4%	102-292	190
170	U00007	39.4%	102-292	190
188	U00008	39.4%	102-292	190
224	U00009	39.4%	102-292	190
246	U00010	39.4%	102-292	190
264	U00011	39.4%	102-292	190
304	U00012	39.4%	102-292	190

Entry	Accession	Score	Pos	Length
2	U00001	39.4%	102-292	190
9	U00002	39.4%	102-292	190
62	U00003	39.4%	102-292	190
58	U00004	39.4%	102-292	190
115	U00005	39.4%	102-292	190
128	U00006	39.4%	102-292	190
170	U00007	39.4%	102-292	190
188	U00008	39.4%	102-292	190
224	U00009	39.4%	102-292	190
246	U00010	39.4%	102-292	190
264	U00011	39.4%	102-292	190
304	U00012	39.4%	102-292	190

Title	Accession	Score	Pos	Length
2	U00001	39.4%	102-292	190
9	U00002	39.4%	102-292	190
62	U00003	39.4%	102-292	190
58	U00004	39.4%	102-292	190
115	U00005	39.4%	102-292	190
128	U00006	39.4%	102-292	190
170	U00007	39.4%	102-292	190
188	U00008	39.4%	102-292	190
224	U00009	39.4%	102-292	190
246	U00010	39.4%	102-292	190
264	U00011	39.4%	102-292	190
304	U00012	39.4%	102-292	190

Organization	Accession	Score	Pos	Length
2	U00001	39.4%	102-292	190
9	U00002	39.4%	102-292	190
62	U00003	39.4%	102-292	190
58	U00004	39.4%	102-292	190
115	U00005	39.4%	102-292	190
128	U00006	39.4%	102-292	190
170	U00007	39.4%	102-292	190
188	U00008	39.4%	102-292	190
224	U00009	39.4%	102-292	190
246	U00010	39.4%	102-292	190
264	U00011	39.4%	102-292	190

[illegible]







Pierce, J.J., Rowan, W.D.  
Plant Physiol. (1993) 103:467-476

#journal  
#title Cloning of higher plant omega-3 fatty acid desaturases.  
#contents cDNA:BND  
#accession PQ0817

#molecule\_type mRNA  
#residues 1-404 #label YAD  
#cross-references Citations

COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.

CLASSIFICATION Report family omega-3 fatty acid desaturase  
AminoAcids oxidoreductase  
SUMMARY #length 404 #molecular-weight 46k17 #sheetsum 9400

Query March 23 19; Score 706; E=1e-16; Length 404;  
Best Local Similarity 31.2%; E=ed. No. 2,756 103;  
Matches 126; Conservative 81; Mismatches 113; Indels 19; Gaps 15;

Db 33 aspicecphqldfdgappfhdadideipbhwtknghmsvyrclav--fala 90  
||||| : | : ||| :::: ||| | : : : :||| :  
QY 10 SPSPKSELDNIKKVPEFETFTWTKATIRHFRGCGIFPGFYIMDIINAFSPYY 69  
Db 91 agaa-y-l-n-hwlpwyiaagttimallvivdhcdqtgsfsdplnsvglhlse 145  
: . . : . : ||| : : : ||| : ||| : : : ||| :  
QY 79 ATTFEELIHRLSTFAVI LVMAGGV VLVNWVAIMECHMAFSIDMETIVGLIEEST 129  
Db 146 llvpynqrishrhbnndhvendeswhpm-se-kiy-kaldkp-triffitlplvm 199  
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :  
QY 130 LUTYEVCYSCHPENCRCCEFEVEVFESRCLFWVTCTHNPLDPTWMLTVGEITLQ 184  
Db 200 la-y-pyl-wars-fghkgshchddslflfnmdtllr-asvt-amovlvnltfrm 256  
: : : : ||| : : ||| : : ||| : : ||| : : ||| :  
QY 190 MPLIAFNVSCHPYDGSAACHHRNRIYNDRHQIYTENGLAVGTGTAAGAAGV 249  
Db 257 gmqklkytyfwytawewdlrtvylnhhjpscklfwyrfkwesylvrgtlrrdyqlino 416  
: : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| :  
QY 250 ASMCYCVALFLNYSLVLALVLTIGT TIPS LNHSNSDLMMECALAVEPVGLNR 397  
Db 317 ihbdl-gthvihhlfpgihpyhvleaetkaakvsykvi 354  
: : ||| ||| ||| ||| :||| :||| :||| :||| :||| :  
QY 238 VFHLHTTRGHAELELYMHWAAASAHILSDLLTG 345

RESULT 7  
ENTRY 7  
TITLE #type complete  
ORGANISM omega-3 fatty acid desaturase (EC 1.1.1.19.-) GM3 - soybean  
#formal name Glycine max Kunitz-like soykan  
#toprap name ksoapomeo revision 2-4ay 1994 from Chicago  
DATE 02-Jun-1994

ACCESSIONS  
J02338  
REFERENCES  
J02338  
AUTHORS Yadao, N.S.; Weitzbach, A.; Angster, M.; Gastor, C.S.; Peter-Gabig, U.; Krings, A.T.; Hirtz, W.O.; Roohifard, O.R.; Schwemmer, B.; Stecker, R.G.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.D.; Russell, S.H.; Feldmann, K.A.; Pierce, J.J.; Browne, J.  
Plant Physiol. (1993) 103:467-476  
Cloning of higher plant omega 3 fatty acid desaturases.  
#accession J02338  
#molecule\_type mRNA  
#residues 1-380 #label YAD  
The omega-6 and omega-3 fatty acid desaturases introduce the second and the third double bonds respectively, in two independent et

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88

[illegible]







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13

QY 259 PLLVNGFVLVLTGCHGCSLPHDSSEWMIKALALATVDRVGLIKKVF-HNITDTH 316

Db 287 IHHVTTAFPPHLETFPPHKLPPH 113

Y 317 VHHLESTHMHAMFATKALPLCEY 344

## RESULT 14

ENTRY

S49331 #type complete

TITLE

n-6 fatty acid desaturase spinach

ORGANISM

#format name Spinacia oleracea #accession name U00001

DATE

16-Feb 1995 #sequence revision 12-May 1995 #text change 12-May 1995

ACCESSIONS

S49331

REFERENCE

S49331

AUTHORS

Schmidt, H.

SUBMISSION

Submitted to the EMBL Data Library, March 1994

ACCESSION

S49331

STATUS

preliminary

MOLECULE TYPE

mRNA

RESIDUES

447 #label CCH

CROSS-REFERENCES

EMBL:X78311

SUMMARY

#length 447 #molecular-weight 51143 #checksum 6764

Query Match

7.98% (size 279, 28 100, 1000h 447)

Best Local Similarity

25.98% (local No. 2, 25e 19)

Matches

79; Conserved 79; Mismatches 115; Indels 26; Gaps 23

Db

127 wotlvslsy alqif-makewyl-plawwtqatqivtvgdchskskkl 183

Y

56 WHILASCTVYVATITTELEWLSYFAMFLPMQGVITQWVLAERGHASSTQW 117

Db

184 wvdlvplafpyfy-ymwltlshhkhlmjrcd-awlnak-dj-ss-eg-1 232

Y

118 LQPTVO-LPHRFELVITFQWYTHFRHRTTHFRFETTHKSDHWKRYLNP 176

Db

238 rks l : yvj fl stx mltkw : kntnlktrpckrfsj : vvfsv 287

Y

177 GRTWLVQFTLQWLYLAFVNSCHPYDGFNFHNPAPLYNDEKQIYISDA-GILA 235

Db

288 lswpllykt-qiywikwlmplgylqstltvhtlaphipkkskemaagql 345

Y

236 VCYGLHYAAVQVWASWVCHGVLLVNGFVLVLTGCHGCSLPHDSSEWMIKAL 245

Db

346 sylvhodyprwlelchds-whiphskipsynlraangslengwy 395

Y

296 A-TYDRVGLIKKVF-HNITDTHVHHLSTHMHAMFATKALPLCEY 344

RESULT 15

ENTRY

S43770 #type complete

TITLE

Delta-12 desaturases - Synecocystis sp. (p006714)

ORGANISM

#format name Synecocystis sp. #accession name p006714

DATE

20-Oct-1994 #sequence revision 20-Oct 1994 #text change 20-Oct-1994

ACCESSIONS

S43770

REFERENCE

S43770

AUTHORS

Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

JOURNAL

Plant Mol. Biol. (1994) 24:643-650

TITLE

Identification of conserved domains in the Delta-12

desaturases of cyanobacteria.

ACCESSION

S43770

STATUS

preliminary

RESIDUES

1-349 #label SAK

Dec 17 11:08

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14

SUMMARY #length 349 #molecular-weight 40340 #checksum 5411

Query Match

7.78% (size 279, 28 100, 1000h 349)

Best Local Similarity

25.98% (local No. 2, 25e 19)

Matches

82; Conserved 82; Mismatches 129; Indels 29; Gaps 23

Db

28 htktpkctekkkaskawavl itlgavvygilylpm ycip-ftw-kt-g 79

Y

35 LKKAAPNHTREDFRSPFQVWHLHAGCTVYATITTELEWLSYFAMFLPMQGV 94

Db

90 yafvfydtpstfokwv-lyzhtstqfhytsswtlthhahhbklevd 139

Y

95 VLTQWVAVFQVWASWVCHGVLLVNGFVLVLTGCHGCSLPHDSSEWMIKAL 154

Db

140 nwdpw-s-wc-a-fasp a ivllyratp-p-fw w tgsilhwqlm hklks 185

Y

150 LFTFEEZGFHWQVYDNLHGLQVYVZSLHMLAFNGVSEFQVFAHQVY 214

Db

186 n-faerdkvklslavfllaafpalittqwgfvklmpwlyhlmsltiv 243

Y

215 MLYVSEHLGFTSEKQZ LANYSLTRVANNVYKMWYVYVTLVTVVYVITVY 273

Db

214 hllpeltfcedwskavagfupzhcdypwewlchds-ndpflkzavafpyat 202

Y

234 ZPCPGRNPHVQGMWMLPQAL AYVQPPYGLDPPVF HNITDTHVHHLSTHMHAM 331

Db

303 lbaslkypwprfye 319

Y

332 FATKALPLCEY YQ 346

Db

Y

Db

Y

Db

Y

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Search completed: Wed Dec 17 11:08:37 1997

Job time : 55 secs.







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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

```
Run on: Wed Dec 17 11:11:11 1997, MasPar time 14.13 Seconds
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Tabular output not generated

Title:	DOI: 10.1186/1745-6215-9-276
Description:	(1-334) English (English)
Page 1 of 1	3009

## Section:

### Scoring table

[illegible]

Post-processing: Minimum Match 0%

Database:

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343:uannn339 344:uannn340 345:uannn341 346:uannn342
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351:uannn347 352:uannn348 353:uannn349 354:uannn350
355:uannn351 356:uannn352 357:uannn353 358:uannn354
359:uannn355 360:uannn356 361:uannn357 362:uannn358
363:uannn359 364:uannn360 365:uannn361 366:uannn362
367:uannn363 368:uannn364 369:uannn365 370:uannn366
371:uannn367 372:uannn368 373:uannn369 374:uannn370
375:uannn371 376:uannn372 377:uannn373 378:uannn374
379:uannn375 380:uannn376 381:uannn377 382:uannn378
383:uannn379 384:uannn380 385:uannn381 386:uannn382
387:uannn383 388:uannn384 389:uannn385 390:uannn386
391:uannn387 392:uannn388 393:uannn389
```

Statistics: Mean 46.671; Variance 103.065; scale 0.455

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Prod. No.
1	792	26.2	379	4	002337	omega-3 fatty acid	4,000-111
2	787	25.0	356	5	004232	omega-3 fatty acid	6,000-111
3	770	25.4	283	5	044227	omega-3 fatty acid	6,000-111
4	727	24.0	319	16	025255	omega-3 fatty acid	6,000-101
5	705	23.5	453	3	002339	omega-3 fatty acid	7,100-101
6	706	23.1	404	5	020812	omega-3 fatty acid	6,000-101
7	693	22.0	380	5	002336	omega-3 fatty acid	5,000-100
8	697	22.0	416	5	002335	omega-3 fatty acid	5,100-101
9	690	22.8	404	14	002400	aspartate delta 15	4,700-100
10	267	6.6	37	16	040711	delta 12 desaturase	7,000-25
11	261	8.6	307	16	040372	delta 12 desaturase	6,810-24
12	245	8.1	447	16	050009	n-6 fatty acid decar	2,700-21

13	234	7.9	55.9	584259	beta(1)-caseinase (	2.36e+01
14	227	7.7	44.7	594331	n-6 fatty acid desat	2.36e+01
15	232	7.5	349.16	583370	Delta-12 desaturase	2.14e+18
16	210	6.9	351.9	515554	stearoyl-CoA desatur	1.02e+15
17	124	4.2	68.9	584800	hydroxy-methylgluta	1.49e+03
18	107	3.5	359.15	585157	beta(4) caseinase	3.36e+01
19	103	3.4	338.12	585160	caseinase (bacterio	2.79e+01
20	102	3.4	555.11	585265	epsilon-N-acetylserine	1.07e+01
21	103	3.4	52.76	584442	hydroxy-methylgluta	2.74e+01
22	99	3.2	33.10	584455	beta(1)-caseinase	2.78e+01
23	100	3.3	234.9	140703	serine protease - 701a	2.14e+01
24	100	3.1	276.4	A42567	serine protease - 701a	2.14e+01
25	100	3.3	437.16	584444	seed protein - Glycyl	2.14e+01
26	100	3.3	437.16	584444	seed protein - Glycyl	2.14e+01
27	101	3.2	722.8	583332	beta(1)-caseinase	1.55e+01
28	98	3.2	149.14	583293	caseinase (bacterio	3.58e+01
29	98	3.2	345.14	584341	caseinase (bacterio	3.58e+01
30	98	3.2	388.14	A55527	oxytocin receptor -	3.58e+01
31	98	3.2	419.14	A54444	oxytocin receptor -	3.58e+01
32	98	3.2	444.11	581990	alpha-galactosidase	3.58e+01
33	96	2.2	485.14	701907	hypothetical protein	5.95e+01
34	98	3.2	532.1	584962	RNA-directed RNA pol	3.58e+01
35	96	3.2	2336.16	A45386	omega-oxo-olixin-sens	5.95e+01
36	94	3.1	77.10	J00435	hypothetical protein	7.9e+01
37	95	3.1	222.14	580745	serine protease (cl	7.64e+01
38	94	3.1	418.14	559601	caseinase (bacterio	9.74e+01
39	92	3.0	136.11	A44554	serine protease (cl	7.03e+01
40	91	3.0	295.9	644114	serine protease - lacto	7.03e+01
41	91	3.0	439.4	517995	serine protease - lacto	7.03e+01
42	92	3.0	477.10	H544210	eggshell protein p48	1.50e+01
43	91	3.0	498.17	700119	4-methylcrotonyl-CoA	2.03e+01
44	91	3.0	435.19	583447	serine protease (cl	7.03e+01
45	92	3.0	965.11	583835	beta(5)-caseinase	1.50e+01

## ALIGNMENTS

```

RESULT      1
ENTRY       J02337
TITLE       cncg-3 fatty acid desaturase (FC 1.14.99.-) RN3 - rapce
            #Format name: classic1 RN3s #Common name: rnc
            35-Sep-1993 #Release: revision 20 Aug 1991 text_chang
            21-Mar-1996

```

ACCESSIONS  
REFERENCE

**Authors** Yabuta, M., K. Watanabe, A. Asanuma, M. Saito, C.S. Yoder, A.J. Kimbey, A.J. Hiltz, W.D. Booth Jr., P. Perez-Grau, L. Kimbey, A.J. Hiltz, W.D. Booth Jr., Schweigler, R.; Staccia, K.L.; Allen, S.M.; Blackwell, Felter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, P.; Pierce, J.; Browne, J.

**Journal** Plant Physiol. (1993) 103:457-476

**Title** Cloning of higher plant omega 3 fatty acid desaturases

[illegible]

##residues 1-377 ##label VAD  
##cross-references GB:122962  
##COMMENT This enzyme initiates the first double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.

## CONTENTS

CLASSIFICATION	Feeder family omniv. 3 fatty acid desaturase
RECORDS	of 1 record, age
SUMMARY	Length 200 mm, total weight 4220 g, fat 16.6 mm, 224



























[illegible]

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MP007036 protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Dec 17 11:00:41 1997; Masp4 time 10.08 seconds

Tabular output not generated.

**Title:** *See the City of A.*  
**Description:** (1384) L.L. 10085, 2007h, p. 2000

## Section 100

Scoring table: PAM 150

Searched: 59021 scgs, 07/10/00 14:44:00

Post-processing: Minimum Match 0%

Database: swiss-prot34

8:part8 9:part9 10:part10 11:part11

Statistic: Mean 48.387; Variance 84.464;  $se = 0.073$

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## Summary

Result No.	Score	Query Match	Length	DB	ID	Description	Prod. No
1	2716	89.9	383	1	EDL6	AMPH-6 FATTY ACID DE	0.66-150
2	2317	76.7	283	3	EDL2	STEAR-6 FATTY ACID DE	0.66-150
3	2173	74.7	367	2	EDL5	MYRIS-6 FATTY ACID DE	0.66-150
4	777	75.7	317	5	EDL3	HEXAD-6 FATTY ACID DE	4.14-149
5	769	75.4	366	3	EDL8	ARACH-6 FATTY ACID DE	0.66-150
6	754	75.0	383	3	EDL7	BEAR-6 FATTY ACID DE	0.88-147
7	725	74.0	380	3	EDL8	PHARO-6 FATTY ACID DE	5.68-138
8	717	73.7	374	3	EDL5	THUR-6 FATTY ACID DE	4.11-137
9	711	73.5	400	3	EDL5	PLUM-6 FATTY ACID DE	1.00-150
10	685	72.7	422	3	EDL5	STEAR-3 FATTY ACID DE	0.66-150
11	682	72.4	414	3	EDL7	BEAR-3 FATTY ACID DE	0.88-147
12	681	72.3	390	3	EDL5	MYRIS-3 FATTY ACID DE	0.66-150
13	678	72.4	414	3	EDL5	ARACH-3 FATTY ACID DE	0.66-150

Dec 17 11:00 /home/fuller/dec97/US-08-572-027A-2.rsp

14	665	22.0	447	5	EDDC SEBIN	OMEGA-3 FATTY ACID DE	4.73e+00
15	655	21.7	435	5	EDDC ARATH	TEMPERATURE SENSITIVE	9.88e-119
16	735	8.4	447	3	FDGC SPLOL	OMEGA-6 FATTY ACID DE	4.13e+29
17	741	9.3	474	3	FDGC SPYQ9	OMEGA-6 FATTY ACID DE	7.73e-28
18	251	8.3	443	3	EDGC SPANA	OMEGA-6 FATTY ACID DE	2.73e+08
19	722	7.3	418	3	FDGC ALPAB	OMEGA-6 FATTY ACID DE	1.77e-22
20	711	7.5	251	3	EDGC SPYD3	FATTY ACID SENSITIVE	2.44e+20
21	98	3.2	386	7	GDYD FIC	CYTOSOL PROTEIN (OT	5.81e-01
22	98	3.2	380	7	GDYD JUMED	CYTOSOL PROTEIN (OT	5.91e-01
23	96	3.2	415	1	SMIL MOJDE	ALPHA-GLUCOSIDASE A	1.07e+00
24	96	3.2	575	1	ASML YEAST	TRANSPARENT PROTEIN S	1.07e+00
25	96	3.2	275	2	CLIM YEAST	C-1-TETRAHYDROFOLATE	1.07e+00
26	94	3.1	275	1	AMSA NITED	AMMONIA MONOXYGENASE	1.99e+00
27	94	3.1	418	1	WALB CHIT	VALENTININ C-1 ACETYL	1.99e+00
28	93	3.1	439	4	GDYD SPYLA	PERMEASIN MEMBRANE	1.99e+00
29	94	3.1	1886	4	SPYD PAT	INTEGRAL MEMBRANE C17	1.99e+00
30	93	3.0	409	4	FAKE FALIL	HAD PHILIPIN PHILIPIN	6.29e+00
31	91	3.0	414	4	CHIR HUMAN	HEPATIC SURFACTANT A1	4.71e+00
32	91	3.0	221	4	CHIR MURIN	HEPATIC SURFACTANT A1	4.71e+00
33	91	3.0	413	1	HZAR HUMAN	HEXA-7-ALDOSE-6-EPIC	4.71e+00
34	90	2.9	419	1	RDAB MECAN	HEXA-7-ALDOSE-6-EPIC	4.70e+00
35	92	2.9	457	4	GDYD CHITR	PROTEIN TRANSDUCER	3.52e+00
36	92	3.0	477	10	YKUS MYCE	HYDROLYTIC PHOSPHOLIP	3.52e+00
37	91	3.0	572	11	GDYD FICPZ	HYDROLYTIC PHOSPHOLIP	4.71e+00
38	90	3.0	572	11	GDYD YEAST	HYDROLYTIC PHOSPHOLIP	4.71e+00
39	91	3.0	409	11	YKUS YEAST	HYDROLYTIC PHOSPHOLIP	4.71e+00
40	91	3.0	443	4	GDYD SPYAW	PROTEIN TRANSDUCER C17	3.52e+00
41	91	3.0	693	9	TDGS MOUSE	PROTEIN-GLUTAMINE C17	4.71e+00
42	90	2.9	792	10	YKUS ESVI	HYDROLYTIC PHOSPHOLIP	6.29e+00
43	91	3.0	1886	4	SPYD PAT	INTEGRAL MEMBRANE C17	1.99e+00
44	91	3.0	2171	2	CLIC PARIT	DIPHOSPHATIDYL INOSIT	4.71e+00
45	91	3.0	221	4	CHIR MURIN	HAD PHILIPIN PHILIPIN	6.29e+00

## ALIGNMENTS

	RESULT	1	
1D	EEAF_AAFCH	STAIRARD;	PPT; 383 AA.
AC	P46513;		
DT	01-NOV-1995 (REFL. 32, CREATED)		
PT	01 NOV 1995 (REFL. 32, LAST SEQUENCE UPDATE)		
DT	01-FEB-1996 (REFL. 33, LAST ANNOTATION UPDATE)		
DE	OMEGA-6 FATTY ACID DEHYDROGENASE, PROPLASMIC RETIUMUM (EC 1.14.99.-)		
SE	(DELTA 12 DECATERASE).		
EN	FAD2.		
OS	ARABIDOPSIS THALIANA (MOORE-EAR CRESS).		
OC	EMBRYONIC, PLANTA, EMBRYONITIS, ANGIOSPERMAY, DICOTYLEDONACEAE,		
CC	CAPRAVALES; CRUCIFERAE.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	SKUFFY I, LIECHTEN I, FRIEMAN K., YANOV N., LAFR E., BRIDGE J.;		
FX	MEDLINE; 9417697.		
FI	PLANT CELL 6:147-158(1994).		
FT	1,5,10,15,20,25,30,35,40,45,50,55,60,65,70,75,80,85,90,95,100,105,110,115,120,125,130,135,140,145,150,155,160,165,170,175,180,185,190,195,200,205,210,215,220,225,230,235,240,245,250,255,260,265,270,275,280,285,290,295,300,305,310,315,320,325,330,335,340,345,350,355,360,365,370,375,380,385,390,395,400,405,410,415,420,425,430,435,440,445,450,455,460,465,470,475,480,485,490,495,500,505,510,515,520,525,530,535,540,545,550,555,560,565,570,575,580,585,590,595,600,605,610,615,620,625,630,635,640,645,650,655,660,665,670,675,680,685,690,695,700,705,710,715,720,725,730,735,740,745,750,755,760,765,770,775,780,785,790,795,800,805,810,815,820,825,830,835,840,845,850,855,860,865,870,875,880,885,890,895,900,905,910,915,920,925,930,935,940,945,950,955,960,965,970,975,980,985,990,995,1000,1005,1010,1015,1020,1025,1030,1035,1040,1045,1050,1055,1060,1065,1070,1075,1080,1085,1090,1095,1100,1105,1110,1115,1120,1125,1130,1135,1140,1145,1150,1155,1160,1165,1170,1175,1180,1185,1190,1195,1200,1205,1210,1215,1220,1225,1230,1235,1240,1245,1250,1255,1260,1265,1270,1275,1280,1285,1290,1295,1300,1305,1310,1315,1320,1325,1330,1335,1340,1345,1350,1355,1360,1365,1370,1375,1380,1385,1390,1395,1400,1405,1410,1415,1420,1425,1430,1435,1440,1445,1450,1455,1460,1465,1470,1475,1480,1485,1490,1495,1500,1505,1510,1515,1520,1525,1530,1535,1540,1545,1550,1555,1560,1565,1570,1575,1580,1585,1590,1595,1600,1605,1610,1615,1620,1625,1630,1635,1640,1645,1650,1655,1660,1665,1670,1675,1680,1685,1690,1695,1700,1705,1710,1715,1720,1725,1730,1735,1740,1745,1750,1755,1760,1765,1770,1775,1780,1785,1790,1795,1800,1805,1810,1815,1820,1825,1830,1835,1840,1845,1850,1855,1860,1865,1870,1875,1880,1885,1890,1895,1900,1905,1910,1915,1920,1925,1930,1935,1940,1945,1950,1955,1960,1965,1970,1975,1980,1985,1990,1995,2000,2005,2010,2015,2020,2025,2030,2035,2040,2045,2050,2055,2060,2065,2070,2075,2080,2085,2090,2095,2100,2105,2110,2115,2120,2125,2130,2135,2140,2145,2150,2155,2160,2165,2170,2175,2180,2185,2190,2195,2200,2205,2210,2215,2220,2225,2230,2235,2240,2245,2250,2255,2260,2265,2270,2275,2280,2285,2290,2295,2300,2305,2310,2315,2320,2325,2330,2335,2340,2345,2350,2355,2360,2365,2370,2375,2380,2385,2390,2395,2400,2405,2410,2415,2420,2425,2430,2435,2440,2445,2450,2455,2460,2465,2470,2475,2480,2485,2490,2495,2500,2505,2510,2515,2520,2525,2530,2535,2540,2545,2550,2555,2560,2565,2570,2575,2580,2585,2590,2595,2600,2605,2610,2615,2620,2625,2630,2635,2640,2645,2650,2655,2660,2665,2670,2675,2680,2685,2690,2695,2700,2705,2710,2715,2720,2725,2730,2735,2740,2745,2750,2755,2760,2765,2770,2775,2780,2785,2790,2795,2800,2805,2810,2815,2820,2825,2830,2835,2840,2845,2850,2855,2860,2865,2870,2875,2880,2885,2890,2895,2900,2905,2910,2915,2920,2925,2930,2935,2940,2945,2950,2955,2960,2965,2970,2975,2980,2985,2990,2995,3000,3005,3010,3015,3020,3025,3030,3035,3040,3045,3050,3055,3060,3065,3070,3075,3080,3085,3090,3095,3100,3105,3110,3115,3120,3125,3130,3135,3140,3145,3150,3155,3160,3165,3170,3175,3180,3185,3190,3195,3200,3205,3210,3215,3220,3225,3230,3235,3240,3245,3250,3255,3260,3265,3270,3275,3280,3285,3290,3295,3300,3305,3310,3315,3320,3325,3330,3335,3340,3345,3350,3355,3360,3365,3370,3375,3380,3385,3390,3395,3400,3405,3410,3415,3420,3425,3430,3435,3440,3445,3450,3455,3460,3465,3470,3475,3480,3485,3490,3495,3500,3505,3510,3515,3520,3525,3530,3535,3540,3545,3550,3555,3560,3565,3570,3575,3580,3585,3590,3595,3600,3605,3610,3		











[illegible][illegible]



CC	AND/OR BE INVOLVED IN METAL ION BINDING.
CC	1- SIMILARITY TO OTHER PLANT OMEGA-3 FATTY ACID ESTERASES.
DR	EMBL: D01418; GI67148; -
KM	OXALOBACILLUS FATTY ACID HYDROLYSING, ENTEROLACTIC BACTERIUM.
KM	TRANSMEMBRANE.
FT	TRANSMEM 43 73 POTENTIAL.
FT	TRANSMEM 219 230 POTENTIAL.
FT	TRANSMEM 234 254 POTENTIAL.
FT	DOMAIN 98 102 HISTIDINE BOX 1.
FT	DOMAIN 134 138 HISTIDINE BOX 2.
FT	DOMAIN 301 305 HISTIDINE BOX 3.
SO	SEQUENCE 383 AA; 4 cysteine; 144/148/147.
	Query Match 75.0% Score 764; E-3 Length 383.
	Best Local Similarity 30.4% Pos. Neg. 100-147.
	Matched 169; Conservativ 60; Mismatch 107; Indels 27; Gaps 14.
Db	25 psagpfgkigdlaalpkhewkspklsmyvridfavaala-maayf----d-sw 77
Qy	1 111:111:111 11 11 111:111:111:111:111:111 11 11
Qy	25 fcehfftwgclakchlfenfkknststclalllao-ryaatffvclmncst 64
Db	78 lmplywaagclfwatvaldhcdqgsdsdplnasvghlshfllypghwstnch 137
Qy	65 amplitmngq-vlqvsvvtnhshhahstvwvcltwvlfncfclvdfcmkysch 144
Db	138 hqthojvcdswpvl--p-ky-khps-rrmytyrplmlyaypylmwspk-- 190
Qy	145 hsnsgkldkdfvfkrrkrrtwwkryknghrrtvyvtyvgt lmplyafnvsrky 203
Db	191 egs---hfrpyslfapseklaetcsinalvylsflvp-zyvkv-ygyypl 245
Qy	204 lscskchshnkakltnkcklqllisa glavvslshraagvawcwvryvdl 261
Db	244 ltmwldavtylhhghokelkpyrgkwswlylgllclidvylfmnhdi-ghvnh 304
Qy	262 lvnghlvdlltldl--lhrs-tnhpschmghsalavldvdyklmkvhnrtldvha 319
Db	305 hlfrpghlvdatsaakhvlygyr 331
Qy	320 hpfstphymeatkrlclgcyq 346
	RESULT 7
ID	FDSE PHAID STANDARD; PRF; 380 AA.
AC	P32291;
DT	01-OCT-1993 (REL. 27, CREATED)
DT	01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DE	01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE	OMEGA-3 FATTY ACID DESATURASE, POMPILASINUS FETIDISSIMUS (PI 1.14.99.-)
DE	(IMIDOLE-3-ACETIC ACID INDUCED PROTEIN ASO).
GN	ARG1.
OS	PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC	PHARANGIOTA; PLANTIA; EMBRYOPHYTA; ANGIOSPERMAE; Dicotyledonales; FABALES;
OC	FABACEAE.
PN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE:HYCOTYL.
RA	YAMAMOTO K.T., MORI H., IMASEKI H.;
RL	PLANT CELL PHYSIOL. 33:13-20(1992).
CC	-1- FINITION: MIPROSEAL (EP) OMEGA-3 FATTY ACID DESATURASE INTERMEDIATES
CC	THE THIRD INTERMEDIATE IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC	IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC	STROMAL AS AN ALTERNATIVE AND TO ACT ON FATTY ACIDS
CC	ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, PROBABLY, OTHER

[illegible]











































































[illegible][illegible]



[illegible][illegible]







CC	FABRICAL.
RN	(1)
RP	SEQUENCE FROM N.A.
CC	TISUO=SEKI;
RX	MEDINE; 94302147.
RA	YANAV N.S., WIERBICKI A., AGEOSTER M., OASTER C.S., PEREZ-GRAD L.,
RA	KINNEY A.J., HITT M.D., ROTH J.R. JR., SCHMIDTTER R., STECCA K.O.,
RA	ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., ROUSSELL S.H.,
RA	REIDMAN R.A., PIERCE J., BROSSE J.J.
RL	PLANT PHYSIOL. 103:467-476(1993).
CC	-1 FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DECARBOXYLase INTRODUCTION
CC	THE THREE DOUBLED IN THE PROSTHETIC OF 16:3 AND 18:3 FATTY
CC	ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANE. IT IS THOUGHT
CC	TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC	ESTERIFIED BY GALACTOLYL-CoA, SULFHYDRIL AND CHROMOPHYLLIDEOLCoA.
CC	-1 PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC	-1 SUBCELLULAR LOCATION: CHLOROPLAST; MEMBRANE-BOUND (PROBABLY).
CC	-1 DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC	AND/OR BE INVOLVED IN METAL ION BINDING.
CC	-1 SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
DR	EMB, 422467; G406792.
DR	PIR_003339; J02339.
KM	OXYDOGENOCLAS; FATTY ACID HYDROXYLASE; CHLOROPLAST; MEMBRANE;
KM	TRANSIT PEPTIDE.
KM	TRANSIT 1.
FT	CHAIN ? 446
FT	CHLOROPLAST (POTENTIAL).
FT	OMEGA-3 FATTY ACID DESATURASE,
FT	DOMAIN 171 175 HISTIDINE BOX 1.
FT	DOMAIN 207 211 HISTIDINE BOX 2.
FT	DOMAIN 374 376 HISTIDINE BOX 3.
SQ	CYSDPPE 493 AA; 93.9% ID; 24.04% ID; 4.0%
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Query March 23 5:53 Score 711 DB 3 Length 453;	
Best local similarity 39.33% Evid. No. 1.76e-124	
Matches 1287 Coverage 74% Identical 192 Indels 22 Gaps 19.	
Dh	98 pgarprlnladiiaarphnecwskdshmyvuvl-gv-tlaaaay--l-n-mtl 150     : : : :           :           :   :   :   :
Qy	25 fteitfftygafahmihetctfegflllmcltlaeyvatvtfllphrlrty 63     : : : :           :           :   :   :   :
Dh	151 wprlyaaqgmfaalivghncdqfstmsklnswghllss[ilpyhgwtstch 210           : : :     :     :     :   :         :
Qy	65 amltymagdyvldwywmlnekmamllawll-wyltlfactatgttcfewtshppa 144           : : :     :     :     :   :         :
Dh	211 hqhghraendeshwp-l-pe-kif-rslcd-vrmrlfrpfllaipvy-l-s-rs- 260   :         : : : : : : : : : : : :   :           :
Qy	145 hgrtslehdrewnykndnkmykfnhdkgwimlvta-p-dmpfladnwacrrp 263   :         : : : : : : : : : : : :   :           :
Dh	261 pyktsgthfpasdlfyprnerkv-ntstaqaamlqlvlvgfwmpgplqlkygyryi 319   :     : : : :   : : : : :   :   : : : :   :           :
Qy	204 poqrachnprradlynrerelddiyfsnatllavcgrdr yaawqvkwscvfotlll 252   :     : : : :   : : : : :   :   : : : :   :           :
Dh	320 twmldlvtylhbhqedklpyrgkwesylvglftcdtygwminlnhdt-qtvnhh 378   :         :   :   :       :           :   :           :
Qy	263 vnsrvllvtlqdh-thrs lprtydsdwmlkhalatvdyoqlnkqfnnltptvwahh 320   :         :     :         :           :   :           :
Dh	379 lfpgldphylvateakpvfgkyyr 404   :         :     :         :   :           :
Qy	321 lrttwywhamatalnakrltseoty 346   :         :     :         :   :           :
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Residue 11	
ID	FD3C BRANA STANDARD; PRT; 404 AA.
CC	P4681ef

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DN DBL; L6296; G43641;
NM OXALIDIBOLANSE; FATTY ACID BIOSYNTHESIS; ENERGETIC; BETA-LAMIN; BETA-AMINO;
FM TRANSMEMBRANE.
FT TRANSMEM 56 76 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 225 245 POTENTIAL.
FT TRANSMEM 252 272 POTENTIAL.
FT DOMAIN 105 109 HISTIDINE BOX 1.
FT DOMAIN 141 145 HISTIDINE BOX 2.
FT DOMAIN 315 319 HISTIDINE BOX 3.
EN DEPEND 363 66; 443 66; 543 66; 643 66; 743 66; 843 66; 943 66; 1043 66; 1143 66; 1243 66; 1343 66; 1443 66; 1543 66; 1643 66; 1743 66; 1843 66; 1943 66; 2043 66; 2143 66; 2243 66; 2343 66; 2443 66; 2543 66; 2643 66; 2743 66; 2843 66; 2943 66; 3043 66; 3143 66; 3243 66; 3343 66; 3443 66; 3543 66; 3643 66; 3743 66; 3843 66; 3943 66; 4043 66; 4143 66; 4243 66; 4343 66; 4443 66; 4543 66; 4643 66; 4743 66; 4843 66; 4943 66; 5043 66; 5143 66; 5243 66; 5343 66; 5443 66; 5543 66; 5643 66; 5743 66; 5843 66; 5943 66; 6043 66; 6143 66; 6243 66; 6343 66; 6443 66; 6543 66; 6643 66; 6743 66; 6843 66; 6943 66; 7043 66; 7143 66; 7243 66; 7343 66; 7443 66; 7543 66; 7643 66; 7743 66; 7843 66; 7943 66; 8043 66; 8143 66; 8243 66; 8343 66; 8443 66; 8543 66; 8643 66; 8743 66; 8843 66; 8943 66; 9043 66; 9143 66; 9243 66; 9343 66; 9443 66; 9543 66; 9643 66; 9743 66; 9843 66; 9943 66; 10043 66; 10143 66; 10243 66; 10343 66; 10443 66; 10543 66; 10643 66; 10743 66; 10843 66; 10943 66; 11043 66; 11143 66; 11243 66; 11343 66; 11443 66; 11543 66; 11643 66; 11743 66; 11843 66; 11943 66; 12043 66; 12143 66; 12243 66; 12343 66; 12443 66; 12543 66; 12643 66; 12743 66; 12843 66; 12943 66; 13043 66; 13143 66; 13243 66; 13343 66; 13443 66; 13543 66; 13643 66; 13743 66; 13843 66; 13943 66; 14043 66; 14143 66; 14243 66; 14343 66; 14443 66; 14543 66; 14643 66; 14743 66; 14843 66; 14943 66; 15043 66; 15143 66; 15243 66; 15343 66; 15443 66; 15543 66; 15643 66; 15743 66; 15843 66; 15943 66; 16043 66; 16143 66; 16243 66; 16343 66; 16443 66; 16543 66; 16643 66; 16743 66; 16843 66; 16943 66; 17043 66; 17143 66; 17243 66; 17343 66; 17443 66; 17543 66; 17643 66; 17743 66; 17843 66; 17943 66; 18043 66; 18143 66; 18243 66; 18343 66; 18443 66; 18543 66; 18643 66; 18743 66; 18843 66; 18943 66; 19043 66; 19143 66; 19243 66; 19343 66; 19443 66; 19543 66; 19643 66; 19743 66; 19843 66; 19943 66; 20043 66; 20143 66; 20243 66; 20343 66; 20443 66; 20543 66; 20643 66; 20743 66; 20843 66; 20943 66; 21043 66; 21143 66; 21243 66; 21343 66; 21443 66; 21543 66; 21643 66; 21743 66; 21843 66; 21943 66; 22043 66; 22143 66; 22243 66; 22343 66; 22443 66; 22543 66; 22643 66; 22743 66; 22843 66; 22943 66; 23043 66; 23143 66; 23243 66; 23343 66; 23443 66; 23543 66; 23643 66; 23743 66; 23843 66; 23943 66; 24043 66; 24143 66; 24243 66; 24343 66; 24443 66; 24543 66; 24643 66; 24743 66; 24843 66; 24943 66; 25043 66; 25143 66; 25243 66; 25343 66; 25443 66; 25543 66; 25643 66; 25743 66; 25843 66; 25943 66; 26043 66; 26143 66; 26243 66; 26343 66; 26443 66; 26543 66; 26643 66; 26743 66; 26843 66; 26943 66; 27043 66; 27143 66; 27243 66; 27343 66; 27443 66; 27543 66; 27643 66; 27743 66; 27843 66; 27943 66; 28043 66; 28143 66; 28243 66; 28343 66; 28443 66; 28543 66; 28643 66; 28743 66; 28843 66; 28943 66; 29043 66; 29143 66; 29243 66; 29343 66; 29443 66; 29543 66; 29643 66; 29743 66; 29843 66; 29943 66; 30043 66; 30143 66; 30243 66; 30343 66; 30443 66; 30543 66; 30643 66; 30743 66; 30843 66; 30943 66; 31043 66; 31143 66; 31243 66; 31343 66; 31443 66; 31543 66; 31643 66; 31743 66; 31843 66; 31943 66; 32043 66; 32143 66; 32243 66; 32343 66; 32443 66; 32543 66; 32643 66; 32743 66; 32843 66; 32943 66; 33043 66; 33143 66; 33243 66; 33343 66; 33443 66; 33543 66; 33643 66; 33743 66; 33843 66; 33943 66; 34043 66; 34143 66; 34243 66; 34343 66; 34443 66; 34543 66; 34643 66; 34743 66; 34843 66; 34943 66; 35043 66; 35143 66; 35243 66; 35343 66; 35443 66; 35543 66; 35643 66; 35743 66; 35843 66; 35943 66; 36043 66; 36143 66; 36243 66; 36343 66; 36443 66; 36543 66; 36643 66; 36743 66; 36843 66; 36943 66; 37043 66; 37143 66; 37243 66; 37343 66; 37443 66; 37543 66; 37643 66; 37743 66; 37843 66; 37943 66; 38043 66; 38143 66; 38243 66; 38343 66; 38443 66; 38543 66; 38643 66; 38743 66; 38843 66; 38943 66; 39043 66; 39143 66; 39243 66; 39343 66; 39443 66; 39543 66; 39643 66; 39743 66; 39843 66; 39943 66; 40043 66; 40143 66; 40243 66
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CC PHOSPHOLIPIDS.  
CC 1. PLANTMA1: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.  
CC 1-1. STRECHLIDAE: LOCATION: ENDOPLASMIC RETICULUM.  
CC 1-2. STRECHLIDAE: THE HISTIDINE BOX REMAINS MAY CONTAIN THE ACTIVE SITE  
CC 1-3. STRECHLIDAE: AND/OR BE INVOLVED IN METAL ION BINDING.  
CC 1-4. FUNCTION: BY ARGIN, ETHYLENE AND WOUNDING.  
CC 1-5. SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.  
CC 1-6. EMBL: D14101 G287562.  
CC 1-7. OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM,  
CC 1-8. OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM,  
CC 1-9. TRANSMEMBRANE.  
CC 1-10. TRANSMEM.  
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CC	FABRICAL.
RK	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-SPECIFIC MEDICINE; 94302147.
KX	MEDLINE; 94302147.
RA	VANAV N.S., MERICIARI A., AGOSTINI M., CATTELL C.S., FERTIGMAN L., KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWELGER B., STECKA R.L., ALLEN S.M., BLACKBELL M., KELLY H.C., CANADY T.O., REISCHL G.H., FELDMANN K.A., PIERCE J.I., GEORGE J.; 68000-1 ;
RE	PLANT PHYSIOLOGY 103:467-476(1993).
-C-	FUNCTION: CHOROXYLAST OMEGA-3-FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLE-BOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERRODOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS SPECIFICALLY TO SATURATED, UNSATURATED AND MONOSATURATED FATS.
C	1. PATHWAY: POLYSATURATED FATTY ACID BIOSYNTHESIS.
C	1.- SUBCELLULAR LOCATION: CHOROXYLAST, MEMBRANE-BOUND (PROBABLY). -1. DOMAIN: THE HISTIDINE BOX MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING.
C	1.- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
DR	EMBL; U22965; 3408347 .
FR	PIR; J02339; J02339.
KM	OXYGENEUTROLASE; FATTY ACID BIOSYNTHESIS; CHOROXYLAST; MEMBRANE TRANSIT PEPTIDE.
FT	TRANSIT 1
ET	DNAID 2
ET	CDAG 344
ET	DOMAIN 171 17% HISTIDINE BOX 1.
ET	ET DOMAIN 207 21% HISTIDINE BOX 2.
ET	ET DOMAIN 374 37% HISTIDINE BOX 3.
SC	SEQUENCE 453 AA, 5136 MD, 1433116 GCCTG.
<hr/>	
Query Match 23.38% Score 705; DB 3; Length 453;	
Best Local Similarity 14.1%; Eval No. 411e 108;	
Matches 129; Conserved % 7; Matrix score 102; Identity 73; Open 19;	
Db	98 pgaapnrladlaiaialkhwkwfwsmgyvrdl-as-fqlaaay-l-n-dwl 150   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	Z5 PCFFTRFVSELEHSHHEEFEEHFSSFCFLDGLACFYVAAYTFNLIHTCF 84            :: :: ::::     ::::     ::::     ::::     ::::     :::
Db	153 wqpywmgagltkn-w-al-yshd-sh-pstscsk-hmwyghllssallrygwgishrth 210            :: :: ::::     ::::     ::::     ::::     ::::     :::
Qy	85 ampkytwcgvct-vawfahdm-mma-a-s-qmvtqv-tt--csyt fcmtygrhm 124             :: :: ::::     ::::     ::::     ::::     ::::     :::
Db	211 hqhghkvndeswhprl-pe-elv-rslrh-gymmlrtappflsa-fpytl-f-s-ts 260   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	145 HSNTGSLEDFEVFNHSASLSMTSLNLHLDELRYMLLVRL-L-WPDLTAFWSGRH 203   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	261 pyklashldpsddlfepmhkh-l-st-acaaaabhllyvg-ftmpyrdlkilyyyrvyl 319   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	204 DGGFAAMAHKLTLNHAKALKLNDAIKTCSTLCSDLR-TAAVQAQAWVFQNDLT 252   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	320 lwmelclvlylhnhghedcklpwrfgksysyllsgitcdidygmimlnhdh-gtnvlhh 378   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	263 vnsdvilvlgdh-thrs-lefydsqwewehrcalvatdnrgchlknyvhnnittvahn 320   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	379 lfpgdiphylvtealeakpvrfgyvr 404   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Qy	321 LFCSNRGVNMATEAETHLEVYG 346   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
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RESULT 11	HOMOLOG SEARCH STANDARD; ERT; 404 AA.
ID	F03C BRANA
NC	E486Ts,

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FT	CHAIN	2	446	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
FT <td>DOMAIN</td> <td>163</td> <td>167</td> <td>HISTIDINE BOX 1</td>	DOMAIN	163	167	HISTIDINE BOX 1
FT <td>DOMAIN</td> <td>199</td> <td>203</td> <td>HISTIDINE BOX 2</td>	DOMAIN	199	203	HISTIDINE BOX 2
FT <td>DOMAIN</td> <td>366</td> <td>370</td> <td>HISTIDINE BOX 3</td>	DOMAIN	366	370	HISTIDINE BOX 3
20	SEQUENCE	446 AA	5177 AA	ERR007372.1

Query Match	42.0%	2,140/5,137	EB 3/1,204th 446
Best Local Similarity	38.1%	Pred. No. 6,27e-166	
Matches	127	Conservative	76; Warm-bloods 119; Inbels 20; Oaps 16

[illegible]

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01 RESULT 14
02 ID FD3C SESIN STANDARD; PRY 447 AA.
03 P48620;
04 DT 01-FEB-1996 (REL. 33, CREATED)
05 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
06 DT 01-FEB-1996 (REL. 33, LAST AMENDMENT UPDATE)
07 C OMEGA-3 FATTY ACID DEHYDRASE, SUBCELLULAR FRACTION (BT 114343-)
08 PADI.
09 C SEQUENCE ANALYSIS (ORIGINAL SOURCE) (UNPUBLISHED)
10 C EUBACTERIAL PLANT; EMBRYONAL AND POSTEMBRY; HYDROPHOBIC;
11 C SCOPHOBIALS; PEDALIAEAE.
12 RN [1]
13 RE SEQUENCE FROM N.A.
14 RC STRAIN-CV. 4294; TIGEST-ORIGIN;
15 RA SHOIJI K.;
16 RL SHIMIZU (APR 1995) TO EMBRYONAL TISSUE DATA BANKS.
17 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DEHYDRASE INTRODUCES
18 CC THE THIRD DOUBLEDOWN IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
19 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
20 CC TO USE, FERREDOXIN AS AN ELECTRON CARRIER AND TO ACT ON FATTY ACIDS
21 CC ESTERIFIED TO GALACTOLYL-LYS, SULFOLYL-LYS AND PHOSPHATIDYLCHOLEROYL.
22 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
23 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
24 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE.
25 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DEHYDRASES.
26 ER EMBL; U2381; G59004; ...
27 ON OXIDOPHOSPHORYLASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE-

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NO	TRANSIT PEPTIDE	CHLOROPLAST (POTENTIAL)
FT	TRANSIT 1	OMEGA 3 FATTY ACID DESATURASE
FT	CHAIN 2	CHLOROPLAST
FT		HISTIDINE BOX 1
FT	MAIN 171	HISTIDINE BOX 2
FT	MAIN 203	HISTIDINE BOX 3
FT	DOMAIN 376	
FT	ANY 447	

Early Match	79.4%	Early	79.1%	CR	7%	Length	447
Best Lo. of Similarity	38.3%	Pred. No.	7,470	101			
Matches	129	Consistent	106	Index	23	Caps	17

[illegible]

RESULT	15	STANDARD	TRY	430 AA.
10	ED3D APATH			
11	P486221			
12	01-FEB-1996 (FEB. 3)			
13	01-FEB-1996 (FEB. 3)			
14	01-FEB-1996 (FEB. 3)			
15	01-FEB-1996 (FEB. 3)			
16	01-FEB-1996 (FEB. 3)			
17	01-FEB-1996 (FEB. 3)			
18	01-FEB-1996 (FEB. 3)			
19	01-FEB-1996 (FEB. 3)			
20	01-FEB-1996 (FEB. 3)			
21	01-FEB-1996 (FEB. 3)			
22	01-FEB-1996 (FEB. 3)			
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100				



CC	TO USE FERROXYGEN AS AN ELECTRON DONOR AND ACT ON FATTY ACID
CC	ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLCHOLINE
CC	1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC	1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC	1- INDUCTION: BY LOW TEMPERATURES.
CC	1- DOMAIN: THE HISTIDINE BOX REMAINS MAY CONTAIN THE ACTIVE SITE
CC	AND/OR BE INVOLVED IN METAL ION BINDING.
DR	1- SIMILARITY: TO OTHER PLANT OMEGA 3 FATTY ACID DESATURASES.
DR	EMBL: L27158; G516045; .
DR	EMBL: U08216; G497219; .
DR	EMBL: D17578; G471093; .
KM	OXYGENOXYLASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM	TRANSIT PEPTIDE.
FT	TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT	CHAIN ? 435 TEMPERATURE SENSITIVE OMEGA-3 FATTY ACID
FT	DESATURASE, CHLOROPLAST.
FT	DOMAIN 156 160 HISTIDINE BOX 1.
FT	DOMAIN 192 196 HISTIDINE BOX 2.
FT	DOMAIN 359 363 HISTIDINE BOX 3.
SQ	SEQUENCE 435 AA; 50136 MW; 76633ED CDS3;

Query Match	22.3%	Score 675;	EB 3;	Length 435;
Best Local Similarity	39.1%;	Prod No 4	96121;	
Matches 131;	Conservative	71;	Mismatches 110;	Indels 23;
			Gaps 17;	

[illegible]







39	2.0	43.1	44	27.7	18.47	Arhopros +3	4	4.0	0.5
40	2.0	44.1	43	27.7	17.40	Arhopros +3	4	4.0	0.5
41	2.0	44.7	42	27.7	17.40	Arhopros +3	4	4.0	0.5
42	2.0	44.7	41	27.7	17.40	Arhopros +3	4	4.0	0.5
43	2.0	44.7	40	27.7	17.40	Arhopros +3	4	4.0	0.5
44	2.0	44.7	39	27.7	17.40	Arhopros +3	4	4.0	0.5
45	2.0	44.7	38	27.7	17.40	Arhopros +3	4	4.0	0.5

## ALIGNMENT'S

RESULT	LOCUS	DEFINITION	ACCESSION	NID
1	H36906	50K bp cDNA clone 180K157.		
	H36908	Arabidopsis thaliana cDNA clone 180K157.		
	H36908			
	9906407			
	EST.			
	Keywords:	cDNA clone 180K157 library lambda P12 strain var Columbia		

ORGANISM  
Arachidopsis thaliana  
Eucalyptus, Eucalyptus, Myrtophyllus, Myrtophyllus, Capitatus,  
Brassicaceae, Arabidopsis.  
seedlings; 2) tissue culture growth roots; 3) germinated plants half  
with 24 hour light cycle, half on 16 hr light, 8 hour dark  
cycles; 4) same plants as 3) for aerial tissue (stems, flowers  
and siliques). The vectors for E. thaliana ZIP box, the cDNA  
inserts were directly cloned with Sal-NdeI arms using oligo dT  
primed cDNA.

REFERENCE	AUTHORS	TITLE	JOURNAL
(bases 1 to 608)	Nemati, T., de Bruijn, F. O., Green, P., Koochstra, K., Kende, H., McIntosh, B., Ching, P. Y., Bialski, H., Somerville, C., Chisholm, M., Retzel, E., and Somerville, C.	Genes galore: a summary of methods for processing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones	Plant Physiol. 106, 1471-1475 (1994)

Contact: Thomas Newman  
McGill Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.  
Lansing, MI  
Tel: 517-353-0854  
Fax: 517-353-9168  
Email: [neuman@pru.msu.edu](mailto:neuman@pru.msu.edu)

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FEATURES
  source      location/qualities
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              /organism="Acetivibrio nitrosum"
              /strain="100157"
              /strain_var="columbia"
BASE COUNT
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ORIGIN

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	Best Local Similarity	80.94%	Fraction Homology			
	Matches	433	Conservative	0	Mismatches	97
					Indels	5
					Gaps	4
Dh	1	CAGCATTATAGCGTCATGCTGTGGTGGTGCGAGTTCTTCTCATCTCCCTCTG	60			
Gy	177	CATCAATAAATCTGCCTTATATACAAACA ACTTA TTTCTTTCTTTCTTTCTTA	236			

Dh  
61 gccctccttcaacttggcttgccacattatgtgctgtgcaggtttgttcctaacgg 120

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RESULT	Z
LOCUS	746832
DEFINITION	10095 Arabidopsis thaliana clone 145C271.
ACCESSION	746832
NID	949806
REFERENCES	
SOURCE	Chen, Steve; Stone, 145C271 library; Lambda PHL3 strain; var. columb.
EST.	
	510 bp
	map
	EST
	17-AUG-1995

procedures of RNA. The mRNA sources were 1) 7 day germinated etiolated plants of *Brassica napus* L. cv. 'Grimm'; 2) the primer RNA isolated from *Brassica napus* L. cv. 'Grimm' after 24 h of cold shock; 3) 7 day germinated etiolated plants of *Brassica napus* L. cv. 'Grimm' after 24 h of cold shock; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRV's lambda Zip-Lox. The cDNA libraries were directed into phages with Sal-Nci arms using oligo-

ORGANISM: *Arabidopsis thaliana*  
 STRAIN: Col-0 (Columbia); Wilmshurst; Wilmshurst; Capra  
 INSTITUTE: Arabidopsis  
 REFERENCE: 1 (bases 1 to 512)  
 AUTHORS: Wang, T., de Paepe, E., Gough, P., Koster, E., Kendra, K.,  
 Moltischi, C., Chikara, S., Gauthier, N., Gervallio, S., Moshayev,  
 R., et al.  
 REPORT: 1 and Gervallio, S.

TITLE	JOURNAL	COMMENT
Transcriptional activity of a set of 11 oncogenes in cells from large-scale partial sequencing of oncogenes. <i>Anticancer Res</i> 1986, 17:41-1975 (1994)		<p>Contact: Thomas Newman  MSU-DOE Plant Research Laboratory  Michigan State University  MSU-DOE PRL, Michigan State University Plant Biology Bldg., E  </p>

LatSing, Mi  
Tel: 517-353-0854























































Dec 17 15:53 /home/fuller/dec97/US-08-572-027A-3.rst

# III

Dec 17 15:53 /home/fuller/dec97/US-08-572-027A-3.rst

12

[illegible]

RESULT	8		
LOCUS	WA3526	534 bp	GENA
DEFINITION	22903 CMA 16 Adenovirus Thailand CMA clone H1027.		EST
ACCESSION	W43526		
NID	0132794		
KEYWORDS	EST.		

ORGANISM *Arabidopsis thaliana*

## REFERENCE 1 (bases 1 to 534)

Author: "Lewin, L., ed. 1944.

McIntosh, L., Onitoge, J., Farkel, N., Somerville, S., Thompson, M., Retzel, E. and Somerville, C.

**TITLE** Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
**JOURNAL** Plant Physiol. 106, 1741-1756 (1994)

MEDLINE 95148729  
COMMENT

Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory

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MSU-DoE-PRL, Michigan State University Plant Biology Bldg., E  
 Lansing, MI

Tel: 517-353-0854  
Fax: 517-353-0160

Tel: 011-333-7100  
Fax: 011-333-7100  
Email: [info@wafar.com](mailto:info@wafar.com)  
Web: [www.wafar.com](http://www.wafar.com)

seq primer: 17.	Location/Qualification
FEATURES	
source	1..534

organisms *Arabidopsis thaliana* /strain "Columbia" (Lundberg, 1990) and *Phaseolus vulgaris* (L.) cv. "Vespa" (Lundberg, 1990) from 3-day-old seedlings. Using 5 µg of polyadenylated mRNA from 3-day-old *Arabidopsis thaliana* (Columbia) seedling hypocotyls as template and oligo d(T) as primer, first strand synthesis was catalyzed by Moloney murine leukemia virus reverse transcriptase (Pharmacia). Second-strand cDNA was made using the procedure of Gubler and Hoffman (1983) except that DNA ligase was omitted. After the second strand

fragment and EcoRI/NorI adaptors (Pharmacia) were ligated  
 to each end. The cDNA was purified from unligated  
 adaptors by spun column chromatography using Sephacryl  
 S 400 and size fractionated on a 10% polyacrylamide  
 mini gel. Size selected cDNAs (3' 4 kb) were removed  
 from the gel using agarase (New England Biolabs),  
 phenol/chloroform extracted and precipitated using 93 M  
 NaAc (pH 7) ethanol. A portion of each cDNA  
 size fraction (0.1 ug) was co-precipitated with 1 ug of  
 1-112-2-11 (Cytosine-phosphate triphosphate, 3'-phosphorylated  
 arms and then ligated in a volume of 4 ul overnight. Each  
 ligation mix was packaged in vitro using  $\phi$ 29 phage (10 fold  
 packaging extract (Stratagene)). We have determined that  
 although first strand cDNA synthesis was carried out using  
 dNTPs almost all of the cDNAs begin to drop from the poly-A  
 tail. The reason for the loss of the poly-A tail is most  
 likely due to lower than anticipated nucleotide levels  
 during the Klenow repair of nipped ends before the  
 addition of linkers (3'-5' exo instead of 5' 3' pol).  
 When this library is used PfuIIse to remove the Affo and  
 Kiebert, J. et al. (1993) Cell 72:427-441.  
 /clone: "HIC127"  
 /clone: lib="CDA-16"  
 /fusion: "Yfe-seedling hypocotyl"  
 /dev: stage="3 day old"  
 c1: 3534  
 141 a 113 c 114 g 145 t 21 others

clone: "HIC12T"

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/clone lib="CD4-16"  
/tissue="yfr="Seedling hypocotyl"
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/dev/stage="3 day old"
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TRIMA

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BASE COUNT	ORIGIN
141 a	113 c
114 q	145 t
21 others	

Quercy Marsh 16.48; Score 189; DB 116; length 534;

Best local similarity 88.6%; Pred. No. 0.00±0.00;  
Matches 249; Mismatched 0; Mismatches 46; Impuls 3; Caps

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World's End is a CDNA library derived from a total population of























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39 22 1.9 362 112 AT559399 A. thaliana transcrib 7.49e-04  
 40 22 1.9 401 167 T10663 57 vegetative meriste 7.49e-04  
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## ALIGNMENTS

RESULT 1  
 LOCUS H36908 608 bp mRNA EST 25 JUL 1995  
 DEFINITION 15037 Arabidopsis thaliana cDNA clone 180K1517.  
 ACCESSION H36908  
 MID 9906407  
 KEYWORDS EST.  
 SOURCE thale cress clone=180K1517 library=lambda-PR12 strain=var columbia  
 vector=lambda Zip lox primer-T7 dye primer Raitel Sal Raitel2-M2  
 lambda PR12 is a cDNA library derived from equal quantities of 4  
 pools of mRNA. The cDNA sources were 1) 7 day germinated etiolated  
 seedlings; 2) tissue culture grown roots; 3) staged plants half  
 with 24 hour light cycle, half on 16 hr light, 8 hour dark  
 rosettes; 4) same plants as 3 but aerial tissue (stems, flowers  
 and siliques). The vector is BR1's lambda Zip-lox. The cDNA  
 inserts were directionally cloned with Sal-Not arms using oligo dt  
 primed cDNA.

ORGANISM Arabidopsis thaliana  
 Eucaryote; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;  
 Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 608)

AUTHORS Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,  
 McIntosh, L., Ohlrogge, J., Raikther, N., Somerville, C., Thomas, M.,  
 Reitel, E. and Somerville, C.

TITLE Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1241-1255 (1994)

## COMMENT

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 Email: 2231stc@idm.ci.msu.edu.

## FEATURES

source location/Qualifiers  
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 /clone="180K1517"  
 /strain="var columbia"  
 126 a 158 c 126 g 118 t 20 others

## BASE COUNT

Query Match 27.2%; Score 314; EB 44; Length 608;  
 Best Local Similarity 80.7%; Freq. No. 0.000000;  
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## RESULT 2

LOCUS 512 bp mRNA EST 17-AUG-1995  
 DEFINITION 18335 Arabidopsis thaliana cDNA clone 145C277.  
 ACCESSION T46832  
 MID 9949806  
 KEYWORDS EST.

SOURCE thale cress clone=145C277 library=lambda PR12 strain=var columbia  
 vector=lambda Zip-lox primer-T7 dye primer Raitel=Sal Raitel2=Not  
 lambda PR12 is a cDNA library derived from equal quantities of 4  
 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated  
 seedlings; 2) tissue culture grown roots; 3) staged plants half  
 with 24 hour light cycle, half on 16 hr light, 8 hour dark  
 rosettes; 4) same plants as 3 but aerial tissue (stems, flowers  
 and siliques). The vector is BR1's lambda Zip-lox. The cDNA  
 inserts were directionally cloned with Sal-Not arms using oligo dt  
 primed cDNA.

## ORGANISM

Arabidopsis thaliana  
 Eucaryote; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;  
 Brassicaceae; Arabidopsis.

## REFERENCE

1 (bases 1 to 512)  
 AUTHORS Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,  
 McIntosh, L., Ohlrogge, J., Raikther, N., Somerville, C., Thomas, M.,  
 Reitel, E. and Somerville, C.

## TITLE

Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones

## JOURNAL

Plant Physiol. 106, 1241-1255 (1994)

## COMMENT

Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRU, Michigan State University, Plant Biology Bldg., E.  
 Lansing, MI  
 Tel: 517-353-0854















QY 553 CAGTACTCTGCTGCTGCTTTTACTAGCTTAAAGCTTGGGGAACCTTAAAGC 612

Db 121 g--g--gttgcttgcttgcttgcttgcttgcttgcttgcttgcttgcttgcttgct 127

QY 613 GAGGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 672

Db 178 cagatatacctctatagcttgcttgcttgcttgcttgcttgcttgcttgcttgcttgct 237

QY 673 CATATATAATTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 732

Db 238 gctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 297

QY 733 GCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 792

Db 298 tctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 357

QY 791 ATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 850

Db 358 tctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 374

QY 861 ATGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 920

RESULT 8 64326 534 bp mRNA EST 21 MAY 1996

LOCUS 22923 004 15 Arabidopsis thaliana cDNA clone library.

DEFINITION M43526

ACCESSION M43526

KEYWORDS EST.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 534)

AUTHORS Newman, T., deBruin, F. J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Ralston, N., Szele, V. L., Thaler, M., Retzel, E., and Somerville, C.

TITLE Genes, proteins, and a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones

JOURNAL Plant Physiol. 106, 1041-1050 (1994)

MEDLINE 95148729

COMMENT

Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
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Fax: 517-353-9168  
Email: 2233tne@msu.edu  
Seq primer: T7.

FEATURES

1..534  
Location/Qualifiers

/organism="Arabidopsis thaliana"

/strain="Columbia"

/note="Vector: pBluescript SK, Site: EcoRI, Site: EcoRI; Using 5 ug of polyadenylated mRNA from 5 day-old Arabidopsis thaliana (Columbia) seedling hypocotyls as template and oligo d(T) as primer, first strand synthesis was catalyzed by Moloney murine leukemia virus reverse transcriptase (Pharmacia). Second strand cDNA was made using the procedure of Gubler and Hoffman (1983) except that DNA ligase was omitted. After the second strand

reaction, the ends of the cDNA were made blunt with Klenow fragment and EcoRI/MscI adapters (Pharmacia) were ligated to each end. The cDNA was purified from unligated adapters by spin-column chromatography using Sephadryl s-500 and size-fractionated on a 15 low melting point mini-gel. Size selected cDNAs (3-6 kb) were removed from the gel using agarase (New England Biolabs), phenol:chloroform extracted and precipitated using 0.3 M KOAc (pH 7.4) ethanol. A portion of each cDNA size-fraction (0.1 ug) was co-precipitated with 1 ug of BamHI (Stratagene) digested, 3'-phosphorylated arms and then ligated in a volume of 4 ul overnight. Each ligation mix was packaged in vitro using Gigapack II gold packaging extract (Stratagene). We have determined that although first strand cDNA synthesis was initiated using dT, almost all of the cDNAs begin 8-10 bp from the poly-A tail. The reason for the loss of the poly-A tail is most likely due to lower than anticipated nucleotide levels during the Klenow repair of 3'-5' ends before the addition of linkers (3'-5' was instead of 5'-3' pol). When this library is used please reference the ABRC and: Kieber, J., et al. (1993) Cell 72:427-441.

/clone="H1217"

/clone="CD4-16"

/fusion\_type="seedling hypocotyl"

/seq\_strategy="3 day-old"

51..534

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others

ORIGIN

mRNA

BASE COUNT 141 a 113 c 114 g 145 t 21 others











Dec 17 15:33 /home/fuller/dec97/US-08-572-027A-5.rst

LOCUS	493269	432 bp	ERRA	EST	OF AUG 1995
DEFINITION	4647 Arabidopsis thaliana cDNA clone 106G107.				
ACCESSION	U00009				
MID	4932631				
KEYWORDS	EST.				
SOURCE	thale cress clone=106G107 library=Lambda PB2 strain=var columbin				

**SOURCE** Male cross-pollinated primary Lambda PR2 strain was collected from 'Lambda Zip-line' 37 day-old plants at 37°C. Lambda PR2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 3 day germinated elongated seedlings; 2) 3 day-old plants from primary 37°C stratified plants; 3) plants with 24 hour light cycle, half on 16 hr light, 8 hour dark; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's Lambda Zip-Box. The cDNA inserts were ligated into the BamHI arms using a 37°C

ORGANISM    Arabidopsis thaliana  
Phenotype    Erucastrum  
Family    Brassicaceae; Arabidopsis  
Genus    Arabidopsis  
Species    Arabidopsis thaliana

REFERENCE  
1 (bases 1 to 43)  
AUTHORS  
Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H.,

McIntosh, L., Ohlroge, J., Pittman, N., Somerville, S., Thresham, M., Retzel, E. and Somerville, C.

JOURNAL  
Plant Physiol., 106, 1241-1248 (1994)  
COMMENT

Contact: Thomas Newman  
MSU DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE PRL, Michigan State University, Plant Biology Bldg., E.  
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Tel: 517-353-0854  
Fax: 517-353-9168  
Email: [22313tch@ldm.cimn.edu](mailto:22313tch@ldm.cimn.edu).

FEATURES	SOURCE	BASE COUNT	ORIGIN
localities/variables	1..433	102 a	29 others
forjatism "At de fons + halmu"	/clone="105G107"	106 c	92 g
/stran="var columnu"		113 t	

[illegible][illegible]

D6	317	ATTAGTGGATGCTGACCTGATGTTCAGCAATGACTCCTTTTGCTGCT	372
G9	181	ATAAAGAGCTCTCGTAAGCAAGAACTAAATACCTCATCTGCTGCT	234

RESULT    14

Accession	U00336	2.6 kb	1996
Definition	Chloro cDNA, partial sequence (F06P1807.11)		
Accession	U00336		
NID	91669336		
Keywords	EST (expressed sequence tag), Chloro mitei (Stratiolaelaps mitei) (F06P1807.11)		
Source	Chloro mitei (Stratiolaelaps mitei) (F06P1807.11)		

development of large-scale and high-throughput assays for RNAi screening.  
clone: pMER1807.1.31

ORGANISM Citrus unshiu

**REFERENCE**

1 (bases 1 to 326)

**AUTHORS**

Ottaviano M.

**AUTHORS:** JOURNAL: *Journal of Management Education*  
**TITLE:** Journal  
**Submitted for Admission:** Submitted (August 1986) to the JME/JMIR Editorial Office.  
**JOURNAL:** Submitted (August 1986) to the JME/JMIR Editorial Office.

of Cellulose, Ohtsu, Shimizu, Shizuoka 424-02, Japan  
(E-mail: ohtsu@cc.ais.ac.jp, ohtsu@cc.ais.ac.jp)  
Fax: +81-543-69-2115

REFERENCE	2 (sites)
AUTHORS	Hasegawa, T., Endo, T., Moriyasu, T., and Umura, M.
TITLE	Expressed Sequence Tags of Citrus Fruit at Rapid Developing Stage

JOURNAL  
COMMENT  
FEATURES

published (1996)  
Professor 'of Yrs Genome Analysis',  
Location/Qualifiers

Source	1-326
Isolate "Citrus unshiu"	
Isolate "Miyagawa wase satsuma mandarin"	
Isolate "Kohji 1807-131"	
Isolate "Jew state" at 1931-2 developing stage"	
Isolate type "juice sat and pulp segment"	
Base count	63 $\pm$ 101 $\pm$ 58 $\pm$ 104 $\pm$
Origin	

	Serotype	Meth.	11	97%	Coverd. 187%	NR 197%	Length 346j
	Bact. local similarity	79.68j	Pred. No.	3,128	225j		
	Matches	207j	Conservative	n/a	Mismatches	84j	Indels 1j Gaps
Dk	16	CGAGGATTCACGGTCAAGTAAGTGTCTTTGTCGCTGGTGCTCCTGCCTGACT	75				
AY	80	GCCGCCATTGAATCATGAAATAAAGAACAATGTAAGAGAACGCTTAAAGCTG	144				

[illegible][illegible]

De	315	gross weight	326
	1		111
cy	384	total weight	396

RESULT 15











































Dec 17 17:37

home/fuller/dec97/US-08-572-027A-7.rst

19

Dec 17 17:37

home/fuller/dec97/US-08-572-027A-7.rst

20

LOCUS T15239 540 bp mRNA EST 28-JUL-1995  
DEFINITION crs834 Ricinus communis cDNA clone pcrs834 similar to plant  
manubriacanth-1orf1 fatty acid desaturase homolog.

ACCESSION T15239

KEYWORDS 9688892

SOURCE EST

castor bean clone pcrs834 library=lamda2APST strain=Bayer 296  
vector=lamda2AP11 primer-T3 Rsite-EcoRI Rsite2-XhoI Poly(A) RNA  
was purified from developing stage III to stage V (Greenwood &  
Bewley, Can. J. Bot. 60:1751-1760, 1982) and sperm plus embryo of  
immature castor fruits. cDNA was synthesized and cloned into  
lambda2AP11 according to the instructions of the manufacturer  
(Stratagene); synthesis was primed from the poly(A) tail, and  
cloned directionally into XhoI (3') and EcoRI (5') sites. In few  
cases, sequence data indicated that this directionality was  
reversed. Partial cDNA clones predominate.

#### ORGANISM

Ricinus communis  
Eucalyptaceae; Euphyphyti; Magnoliophyta; Magnoliopsida; Rosidae;  
Euphorbiales; Euphorbiaceae; Ricinus.

1 (bases 1 to 540)

#### REFERENCE

van de Loo, F.J., Turner, S. and Somerville, C.  
Expressed sequence tags from developing castor seeds  
Plant Physiol. 108, 1141-1150 (1995)

#### COMMENT

Contact: Somerville CR  
Carnegie Institution  
Carnegie Institution, 290 Panama St., Stanford, CA 94305  
Tel: 4153251521  
Email: crs@andrew.stanford.edu  
Location/Qualifiers

#### FEATURES

Source

1..540  
/organism="Ricinus communis"  
/clone="pcrs834"  
/strain="Baker 296"

BASE COUNT 132 a 104 c 134 g 146 t 24 others  
GC10%

#### Query Match

11.3%; Score 131; DB 55; Length 540;  
Best Local Similarity 71.6%; Fred. No. 1,946 212;

Matches 232; Conservative 0; Mismatches 90; Indels 2; Gaps 2;

DB 79 tctatgggtgcatgttgcattgttcaactttcccttgcattgacacacatttggag 138

YY 764 tctatgggtgcatgttgcattgttcaactttcccttgcattgacacacatttggag 723

DB 139 aacatcaaacagctattccacgtatggtcattcaggaatggattggctcggggagaaa 198

YY 824 aacatcaaacagctattccacgtatggtcattcaggaatggattggctcggggagaaa 883

DB 199 tgggtgcttgcagatagatattatgggttggatgaataagattatccatgaattgggaga 258

YY 884 tgggtgcttgcagatagatattatgggttggatgaataagattatccatgaattgggaga 943

DB 259 ctcatatggtcattcattgttgcattgacgtacattacacatgaatggaggaggaacta 318

YY 944 ctcatatggtcattcattgttgcattgacgtacattacacatgaatggaggaggaacta 1003

DB 319 aaggaatcaaggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 377

YY 1004 aaggaatcaaggaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 1063

DB 378 catgtggaggagg-caaaggagt 400

YY 1064 catgtggaggagg-caaaggagt 1087

Crash to program: 14 Dec 17 17:37:37 1997  
Job time : 725 secs.







[illegible][illegible]



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QY	324	ctccacacaccttccacacacacacacacacacacacacacacacacacacac	388
D6	307	ctctccctccctccctccctccctccctccctccctccctccctccctccctcc	366
QY	384	ctctccctccctccctccctccctccctccctccctccctccctccctccctcc	442
D6	367	ctggcgatccctccctccctccctccctccctccctccctccctccctccctcc	423
QY	443	ctggcgatccctccctccctccctccctccctccctccctccctccctccctcc	502
D6	426	aggggaaatnctaaacacactttgg	451
QY	503	agggaatnctaaacacactttgg	529

[illegible][illegible]

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RESULT: 4
AC ATATGCG CCAATG; PNA; EST: 468 BP.
AF TGAATG
AI 993638
DT 01-APR-1995 (Rel. 43, Created)
DT 12-MAR-1997 (Rel. 51, last updated, Version 16)
TF 1998 At 14:15:33, Thu Apr 9 1998, clone 15401577,
KW EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryota; Eukaryota; Embryophyta; Magnoliophyta;
OC Magnoliopsida; Euphorbiales; Brassicaceae; Arabidopsis.
RP 1-488
RX MEDLINE; 95148729.
RA Norman T., deBorja F.D., Green P., Kocuturk K., Kende H.,
RA Maitshik E., Cheltopo I., Bakhlev V., Somerville S., Thomasow M.,
RA Reisel E., Somerville C.
RA "Gene" is a library of cDNA-clones for accessing results from
RT large-scale partial sequencing of anonymous Arabidopsis cDNA
RT clones;
RI Plant Physiol. 106:1741-1755(1994).
CC Contact: Thomas Norman M.D. Plant Research Laboratory Michigan
CC State University MSU-POR-PIL, Michigan State University Plant
CC Biology Bldg., E. Lansing, MI Tel: 517 353 0854 Fax: 517-353-9168
CC Email: 2031@msu.edu; tnorm@msu.edu; M981 353 464708
FH Key Location/Qualifiers
FH source 1..488
FH organism "Arabidopsis thaliana"
FH clone="15401577"
FH strain "var Columbia"
FH note="thale cress"
FH 1-488 5' end of 127 of 13 other
Query March 21 78; Cope 750; DB 77; length 488;
Best Local Similarity 81 78; Pied No 0.00e+00;
Matches 309; conservative 0; Mismatches 59; Indels 1; Gaps 17

```











[illegible]

RESULT	8	standard; cDNA, EST, 364 bp.
ID	AT1067	
AC	T46100,	
DI	9934331	
DT	10-FEB-1995 (rel. 4z, created)	
DT	12-MAR-1997 (rel. 51, last updated, Version 16)	
DE	9343 Arabidopsis thaliana cDNA clone 13017.	
KW	EST	
OS	Arabidopsis thaliana (thale cress)	
OC	Eukaryota; Eukaryota; Viridiplantae;	
OC	Charophyta; Embryophyta group; Embryophyta; Magnoliophyta;	
OC	Magnoliopsida; Vaparieae; Brassicaceae; Arabidopsis.	
RN	[1]	
RP	1-364	
RA	MELTING, 9614879.	
RA	Newman T., deBrijn F.J., Green E., Kuytendaal K., Kinde H.,	
RA	McIntosh L., Ohlroge J., Baithe N., Copeland M.,	
RA	Reisel E., Somerville C.	
RT	*Genes galore: a summary of methods for accessing results from	
RT	large-scale partial sequencing of anonymous Arabidopsis cDNA	
RT	clones*;	
RT	plant Physiol. 106:1241-1255(1994).	
DB	AG13, T46100, AG13 July 1997.	
CC	Contact: Thomas Newman MGH-ECF Plant Research Laboratory Michigan	
CC	State University MGH-ECF-PRL, Michigan State University, Plant	
CC	Biology Bldg, E. Lansing, MI Tel: 517-487-0804 Fax: 517-487-0168	
CC	Email: 2231rcn@lcm.cmu.edu, NMR1 g1: 94337	
CH	Key	Location:Quiliffors
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FT		/organism="Arabidopsis thaliana"
FT		/clone="130177"
FT		/strain="var columbia"
FT		/note="thale cress"
Q	Sequence 364 bp; K1 A; K1 F; 19 of 4; 4; T; 16 other;	

[illegible]

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QY 931 AAAAAAAAAAAAAAAAAAAAAAAAAA 959
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RESULT	9
ID	ATT14176 standard: RNA, EST, 310 BP.
AC	T14176;
IN	931129
DT	07-MAR-1997 (rel. 38, created)
PT	12-MAR-1997 (rel. 51, last updated, Version 1)
DE	2341 Arabidopsis thaliana cDNA clone 48F127.
KW	EST.
OS	Arabidopsis thaliana (thale cress)
OC	Fukuyama et al. mitochondrial cytochrome c; Viridiplantae;
GC	Charophyta/Euhydropyta group; Embryophyta; Magnoliophyta;
GN	Magnoliopsida; Euphorbiales; Brassicaceae; Arabidopsis.
RP	1-310
RA	MEFELINP; 95145729.
RA	Newman T., Deborah F.J., Green P., Keesstra K., Kendra H.,
RA	McIntosh L., Ollivierre J., Raitheal N., Somerville S., Thomasow M.,
RA	Ratzeal F., Somerville C.;
RT	*Genes selected a summary of methods for accessing results from
RT	large-scale partial sequencing of anonymous Arabidopsis cDNA
RT	clones;
RI	Plant Physiol. 106:1241-1255(1994).
DN	AG15, 114176; AG15 July 1995.
CC	Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan
CC	State University MSU-DOP-PL, Michigan State University Plant
CC	Biology Bldg., East Lansing MI 48824-1312-463-6854 Fax: 517-453-9168
CC	E-mail: 2281@msu.edu; tnewman@MSU.GIT 45170
EH	Key
EH	Location/Qualifiers
FT	source
FT	1..310
FT	/organism "Arabidopsis thaliana"
FT	/clone="48F127"
FT	/strain="var columbiana"
FT	/note="thale cress"
FT	Sequence 310 BP; 73 A; 85 C; 65 G; 83 T; 4 other;

[illegible]



N1	91269060
DT	19-APR-1996 (Rel.47, Created)
DT	12-MAR-1997 (rel. 51, Last updated, Version 9)
DE	21887 Arabidopsis thaliana cDNA clone CDR37.
KM	EST.
RN	
RP	1-432
RA	MEDLINE; 9614879.
RA	Pennan T., deBrujn F.J., Green E., Koppitz R., Koth-B.,
RA	McIntosh L., Chlupp J., Bittorf R., Gervillat S., Thaler M.,
RA	Rezel E., Somerville C.
RT	*Genes cloned: a summary of methods for accessing results from
RT	large-scale partial sequencing of anonymous Arabidopsis cDNA
RL	clones?.
RL	Plant Physiol. 106:1241-1255(1994).
CC	Contact: Thomas McPherson, Plant Research Laboratory Michigan
CC	State University MSU DOE lab, Michigan State University Plant
CC	Biology Bldg.,E. Lansing MI Tel.: 517-353-0814 Fax: 517-353-9168
CC	Email: 2231chen@chem.msu.edu, NCBI gi: 1269060
FH	Key location/Qualifiers
FT	source 1..432
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FT	/clone="G7837"
FT	/strain="columbia"
FT	/note="thalia cross"
FT	mRNA 1..432
SQ	Sequence 432 bp, 119 A, 100 C, 70 G, 122 T, 16 other;
Query Match	13.3%, Score 153; DB 76; length 432;
Best Local Similarity	79.0%, full matrix 72;
Matches	228; Conservative of mismatches 54; Indels 6; Gaps 6;
Dh	144 tcaaatattgttgtaagctgtagacacctcttgcgaactccgtcggtttctac 203       
Cp	1155 ttataaaatttatgtttggtaaataaaaatatttttttttaatttccttccttccttaca 1046 
Dh	204 atgatcacactcttgccctcatataaacgataataaacaggctgccatggatg 263       
Cp	1095 aaatatacaatctctctctctctctctctctctctctctctctctctctctctctctct 1036 
Dh	264 gtatagtctctccagagatggtttatgacctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 123       
Cp	1036 aatatattcttcacatattctctctctctctctctctctctctctctctctctctctctct 977 
Dh	324 ggcatttgtcggaagacagtgtgatgtccagtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 383       
Cp	976 c caatctcagaacacaaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 920 
Dh	384 ttgtttaangtcctngtngtntgtgttngnngnagccaaagttccat 431       
Cp	919 t-ctttAACATTC-GAGAGTGGTAAAGGAAG AAACCTCCTT 874
RESULT	11
ID	AT6393 standard; RNA; EST; 433 BP.
Ac	T226397
N1	993253.
DT	27 JUN 1994 (rel. 49, Created)
DT	12-MAR-1997 (rel. 51, Last updated, Version 15)

[illegible]



















Db	247	tcacacagatcagagacacacacagatgagatgagacagatggtctatctcttcac	306
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Gy	384	ctctctctctctctctctctctctctctctctctctctctctctctctctctct	442
Db	347	ctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	425
Gy	443	ctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	502
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[illegible][illegible]

RESULT	4	strand1, RNA, EST, 488 BP.
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DT	01-APR-1995 (Rel. 43, Created)	
ET	12-MAR-1997 (Rel. 51, Last updated, Version 15)	
DE	12168 Arabidopsis thaliana cDNA clone 15601517.	
RF	EST.	
CC	Arabidopsis thaliana (thale cress)	
OC	Eukaryote, eukaryotic eukaryotes; Viridiplantae;	
NC	Embryophyta; Embryophyta group; Embryophyta; Monocotyledonae;	
GN	Monocotyledonae; Euphorbia; Rosales; Rosaceae; Arabidopsis.	
GI	[1]	
RP	1-488	
RA	MEDLINE; 93148729.	
EA	Newman TG, deHoff Jn P.J., Green P., Koestera K., Rondo H., Mittelman D., Chabrier C., Bialski H., Somerville C., Thompson M., Reichel E., Somerville C.;	
RT	Repeats: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones?;	
RL	Plant Physiol. 106:1241-1255(1994) .	
CC	Contact: Thomas Newman MSU-DGE Plant Research Laboratory Michigan State University MSP-PH-PH, Michigan State University Plant Biology Bldg., Lansing, MI 48911-517-553.0854 Fax: 517-553.9168	
CC	email: 22317-mblwr@climex.msu.edu, NPGI gi. 934308	
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[illegible][illegible]































[illegible]

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DT	12-MAR-1997 (Rel. 51, Last updated, Version 16)		
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KM	EST.		
O5	Arabidopsis thaliana (thale cress)		
OC	Eukaryotes; mitochondrial eukaryotes; Viridiplantae;		
OC	Charophyta/Embryophyta; Equisetum, Liliopsida, Magnoliopsida;		
OC	Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.		
RN	(1)		
RN	1-509		
RX	MEDLINE; 95148729.		
RA	Newman T., deGrujth J.F.J., Green P., Koopmans A., Krogh H.,		
RA	McIntosh L., Ohlrogge S., Falkner N., Somerville S., Thomashow M.,		
RA	Reisel E., Somerville C.;		
RT	"Genes values": a summary of methods for accessing results from		
RT	large-scale partial sequencing of libraries. Arabidopsis cDNA		
RT	clones";		
RL	Plant Physiol. 106:1241-1256(1994).		
DR	AGIS; T452457; AGIS July 1995.		
CC	Contact: Thomas Newman, Wm. Foltz Plant Biotech Laboratory, Michigan		
CC	State University, MSU-DBS Bldg., Michigan State University, East		
CC	Lansing, MI 48246. Tel.: 517 353 0854 Fax: 517 353 9168		
CC	Email: 2233ctcm@dm.climsu.edu, NBI 91: 933654		
FH	key	location/gene/trans	
FT	source	1..509	
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FT		/clone "K8LH7"	
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[illegible]

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RESULT 4
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AI T04093;
NI 3315253
DT 30-AUG-1993 (rel. 36, Created)
DT 12-MAR-1997 (rel. 51, last updated, Version 15)
FE 43 Arabidopsis thaliana cDNA clone S10707P.
KW EST.
OS Arabidopsis thaliana (thale cress)
OC Eukaryota; Metazoa; Chordata; Euteleostomi;
OC Actinopterygii; Cyprinodontiformes; Poeciliidae;
OC Mniastomatidae; Apocarideae; Brassicaceae; Arabidopsis.
RN [1]
RP 1-386
PY MARCHER, G.;APR70A.
RA BROWN, T., JAGGARD, P. L., GREEN, F., KOSTERKA, K., KENDE, H.,
RA MELTZOFF, L., OHLIDGE, J., RATHKE, N., SOMERVILLE, S., THOMASOW, M.,
RA RADICAL, E., SOMERVILLE, C. J.
RT Genes gained a summary of methods for accessing results from
RT large scale partial sequencing of anonymous Arabidopsis cDNA
RT clones?
PL Plant Physiol. 106:1241-1256(1994).
PI 91
DR ACCESSION: A015 JULY 1995.
CC Contact: Thomas Newman MW-DOE Plant Research Laboratory Michigan
CC State University MW-DOE TEL: Michigan State University Plant
CC Biology Bldg. East Lansing MI 48824 FAX: 517/353-9168
CC Email: 2021@msu.edu;tmnew@MSU.GIF 310 310553
KW localization/Qualifiers
SOTIHO 1-386
FT FT /organism="Arabidopsis thaliana"
FT FT /accession="S10707P"
FT FT /strain="var columbiana"
FT FT /note="thale cress"
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19	U00098.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
20	U00099.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
21	U00100.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
22	U00101.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
23	U00102.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
24	U00103.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
25	U00104.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
26	U00105.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
27	U00106.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
28	U00107.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
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33	U00112.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
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37	U00116.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
38	U00117.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
39	U00118.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
40	U00119.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
41	U00120.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
42	U00121.1	16S rRNA	<i>Escherichia coli</i>	ATCC 8739	1542	50.8	GenBank
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Dec 17 15:44 /home/fuller/dec97/US-08-572-027A-5.rst2

10

[illegible][illegible]



## II

Dec 17 15:44 /home/fuller/dec97/US-08-572-027A-5.rst2

12

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Cc      946 GTAAATTCCTAACGTTTGCTTAACCGTAAAACCAAGTCCTCATCAAATTCATCAT 860

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DT   10-FEB-1995 (Rel. 42, created)
DD   12 MAR 1997 (Rel. 57, last updated, version 16)
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KW   EST.
OS   Arabidopsis thaliana (Chen cross).
OC   Eukaryotes; mitochondrion eukaryotes; Viridiplantae;
QC   Charophyta/Empyophyta group Empyophytia/Magnoliophyta;
MC   Magnoliopsida/Capparidae/Sisymbriaceae/Arabidopsis.
RN   [ ]
RP   1-364
RX   MEDLINE; 95148729.
RA   Newman T., deBuijn F.D., Green P., Neegista K., Rende H.,
RA   McIntosh L., Ohlrogge J., Richel N., Somerville S., Thomas M.,
RA   Rezel E., Somerville C.,
RT   Genes galore! a summary of methods for accessing results from
RT   large-scale partial sequencing of anonymous Arabidopsis cDNA
RT   clones?
RL   Plant Physiol. 106:1241-1255(1994).
DR   AGS; T46100; AGS July 1995.
CC   Contact: Thomas Newman Med-Lab Plant Research Laboratory, Michigan State University Plant
CC   State University MSU-DOE FLR, Michigan State University,Plant
CC   Biology Bldg./E Lansing MI Tel: 517 353-0864 Fax: 517-353-9168
CC   Email: 223jtn@ilim.msu.edu yep: jn 04d337
FH   Key location/Qualifiers
FT   source               1..364
FT                         /organism="Arabidopsis thaliana"
FT                         /clone "J35157"
FT                         /strain "Var Columbia"
FT                         /note "Thale cress"
FC       /note="Thale cress"

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DB      73 tggatagcttccccctaaggaagagcccgttatcataagaaatnonitctgtttgac 132
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DB      133 actaatctgaggaagatctatccctgtgtgactaggttaaacaagatgagtgaggacg 192
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DB      193 ctcaaaggagcttggctacccgaaagcaagactacggatatccaacaaaaggtagtccac 252
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Tp      253 aaatctcaaggtgcagagtggtggtatgagggc 284
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[illegible]



























Matches	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100							
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7

Dec 17 17:43 /home/fuller/dec97/US-08-572-027A-7.rsl2



Matches	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100							
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

**Sequence** 486 H<sub>1</sub>, 10<sup>2</sup> A<sub>1</sub>, 1A<sup>+</sup>, 7<sup>-</sup>, 1B<sup>+</sup>, G<sub>1</sub>, 13<sup>+</sup> m; 19-ether.

Query Match: 21.1%; Score: 244; PR: 77; Length: 488;  
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[illegible]

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D7 247 tacttccttcggttgttatcggtgatcaaaatactctgtatctaatcttaccctc 306

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||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||  
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standard, PNA, EST, 488 bp.  
7884727

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AC	T22852;
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01 APR 1995 (Rel. 43, Created)  
12 MAR 1997 (Rel. 51, Last updated, Version 16)  
12168 Arabidopsis thaliana cDNA clone 15601577.

DT 30-JUN-1994 (Vol. 40, created)  
 DT 12-MAR-1993 (Vol. 41, last updated, Version 15)  
 DE 4866 Arabidopsis thaliana cDNA clone 1011b1577.

Arabiopsis thaliana (thale cress)  
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Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

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06 Eukaryotae; mitochondrial eukaryotes; Viridiplantae;  
06 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

1-488  
MEDLINE; 95148729.

RN [1]  
RP 1-528  
PX MESTINP; 95148729.  
R 1-528

McIntosh L., Chittoge J., Finkiel N., Somerville S., Thresham M., Retzel E., Somerville C.;  
 "Genes gained: a summary of methods for accessing results from"

RA McInosh E., Ohlroge J., Kaimel N., Somerville S., Thomasow M.,  
Ketzal E., Somerville C.;  
\*Genes galore: a summary of methods for accessing results from  
large-scale functional genomics experiments  
PT

Plant Physiol. 106:1241-1255 (1994).  
Contact: THOMAS NORMAN MIST DOE Plant Research Laboratory Michigan State University, East Lansing, MI 48824-1324. E-mail: mist@msu.edu

RI *Clomoxyl*  
RL Plant Physiol. 106:1241-1255 (1994).  
DP  
DP AGIC: 222852; AGIC July 1995.  
CC Contact: Thomas Newman MRI-102E Plant Research Laboratory Michigan

Biological Sciences, Lansing, MI tel: 517-353-0874 fax: 517-353-4116  
Email: 22313@mcilbm.climu.edu, NCBI q1: 936308

CC	State University New York, Binghamton State University, Binghamton, NY 16902-6000
CC	Biology Bldg., E. Lansing, MI Tel.: +1 734-0884 Fax: +1 734-9188
CC	Email: 2213@andlcm.csl.msu.edu; NMI g: 932668
TH	Key Location/Qualifiers

```

source
1:400
/analysis "Analysis charting"
/clone="1560157"
/strain="var columbia"

```















[illegible]

RL	clones*?
AT	Plant Physiol. 106:1241-1255 (1994).
CC	Contrib. Thomas Newman Kennel Plant Research Laboratory Michigan
CC	State University Mich-Gaither, Michigan State University Plant
CC	Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517 353 9168
CC	Email: 2237@msu.edu clmsu@msu.edu, NCBI gtr: 95535
FT	Key
FT	Location/Qualifiers
FT	source
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FT	/organism "Arabidopsis thaliana"
FT	/clone="146M127"
FT	/strain "var. columbiana"
FT	/note="holey cross"
FT	Exp.-no. 147 exp. 24 At 78 of 78 of 20 of 13 other?
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Best Local Similarity	78.4% Pred. No. 6,90e-139,
Matches	1497 conservative 07 Mismatches 377 Indels 3, Gaps 3,
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QZ	139 aaggggggggggggggggggggggggggggggggggggggggggggggggggg 256
QY	1 AAAAAAAAAAAAAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QZ	139 aaggggggggggggggggggggggggggggggggggggggggggggggggggg 318
QY	121 AAAAAAAAAAAAAAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
Db	319 annot 323
QY	178 ATCAT 182
RESULT 14	
LOCUS	EMAPSTS 156 bp DNA
DEFINITION	E. miranogaster STS determined from European Mapping Project
ACCESSION	270880
NID	g1263794
KEYWORDS	sequence tagged site,
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
REFERENCE	Elavsky J et al. mitotic effect of embryonic M <sup>2</sup> on the Arthropod
ATTORNS	Insectal Insectal Flycatcher Experiment, Washington, DC
TITLE	Physiology of Insectal Insectal Flycatcher Experiment
INTERNAL	1 (bases 1 to 166)
REFERENCE	European Cross-Phylogenetic Mapping Consortium.
ATTORNS	Submitted (15 Apr 1996) Michael Ashburner, Department of Genetics
TITLE	Downing St., Cambridge CB2 3EH, England
INTERNAL	ST5_name = Dm36375
COMMENT	clone name = 3607
INTERNAL	seq from primer = SP6
INTERNAL	vector class = cosmids, Lister 6
INTERNAL	origin of clone = Oregon R
INTERNAL	in situ site primary = 98C
INTERNAL	BLAST program = BLASTN
INTERNAL	database searched = EMBL
INTERNAL	date of search = 08.01.1996
INTERNAL	BLAST program = BLASTX



